

FIG.1A.

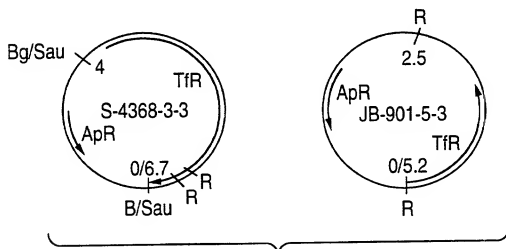


FIG.1B.

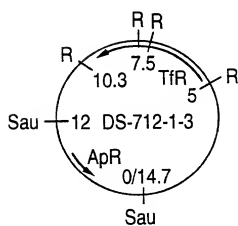


FIG.1C.

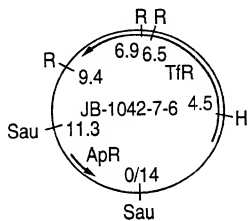


FIG.1D.

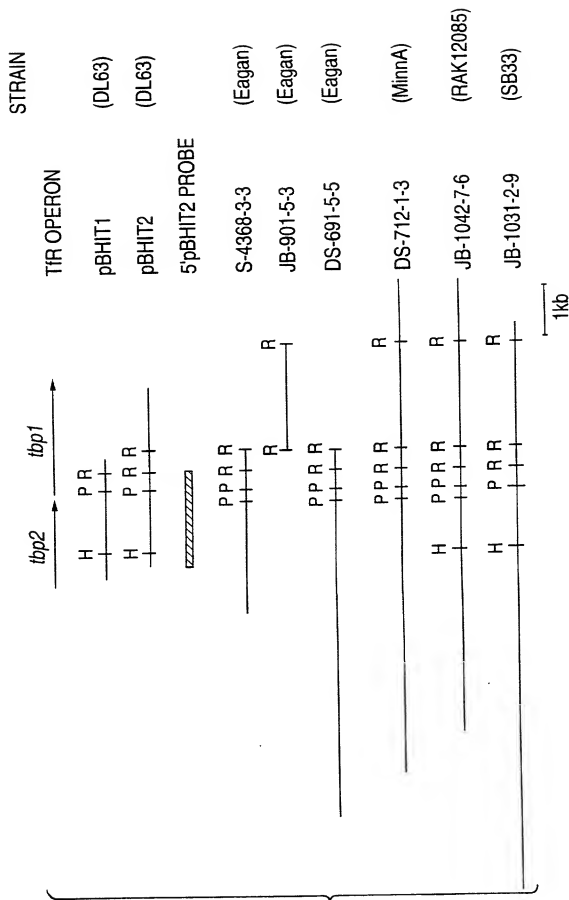


FIG.2.

FIG.3A.

TATTACTCA ATG AAA TCT GTA CCT CTT ATC TCT GGT GGA CTT TCC TTT
Met Lys Ser Val Pro Leu Ile Ser Gly Leu Ser Phe
 1 5 10

TTA CTA AGT GCT TGT AGC GGA GGG GGT TCT TTT GAT GTA GAT AAC GTC
Leu Leu Ser Ala Cys Ser Gly Gly Gly Ser Phe Asp Val Asp Asn Val
 15 20 25

TCT AAT ACC CCC TCT TCT AAA CCA CGT TAT CAA GAC GAT ACT TCA AGT
 Ser Asn Thr Pro Ser Ser Lys Pro Arg Tyr Gln Asp Asp Tyr Ser Ser
 30 35 40 45

TCA AGA ACA AAA TCT AAA TTG GAA AAG TTG TCC ATT CCT TCT TTA GGG
 Ser Arg Thr Lys Ser Lys Leu Glu Lys Leu Ser Ile Pro Ser Leu Gly
 50 55 60

GGA GGG ATG AAG TTA GGG GCT CTG AAT CTT TTT GAT AGG ALC AAA CCT
 Gly Gly Met Lys Leu Ala Ala Leu Asn Leu Phe Asp Arg Asn Lys Pro
 65 70 75

AGT CTC TTA AAT GAA GAT AGC TAT ATG ATA TTT TCC TCA CGT TCT ACG
 Ser Leu Leu Asn Glu Asp Ser Tyr Met Ile Phe Ser Ser Arg Ser Thr
 80 85 90

FIG.3B.

ATT GAA GAG GAT GTT AAA AAT GAC AAT CAA AAC GGC GAG CAC CCT ATT
 Ile Glu Glu Asp Val Lys Asn Asp Asn Gln Asn Gly Glu His Pro Ile
 95 100 105

GAC TCA ATA GTC GAT CCT AGA GCA CCA AAT TCA AAC GAA AAT CGT CAT
 Asp Ser Ile Val Asp Pro Arg Ala Pro Asn Ser Asn Glu Asn Arg His
 110 115 120 125

GCA CAA AAA TAT GTA TAT TCA GGG CTT TAT TAT ATT CAA TCG TCG AGT
 Gly Gln Lys Tyr Val Tyr Ser Gly Leu Tyr Tyr Ile Gln Ser Trp Ser
 130 135 140

CTA AGA GAT TTA CCA AAT AAA AAG TTT TAT TCA GGT TAC TAT GCA TAT
 Leu Arg Asp Leu Pro Asn Lys Lys Phe Tyr Ser Gly Tyr Tyr Gly Tyr
 145 150 155

GGG TAT TAC TTT GGC AAT ACA ACT GGC TCT GCA TTA CCT GTA GGT GGC
 Ala Tyr Tyr Phe Gly Asn Thr Thr Ala Ser Ala Leu Pro Val Gly Gly
 160 165 170

GTA CCA ACG TAT AAA GCA ACT TCG ACC TTC ATC ACC GCA GCT GAA AAT
 Val Ala Thr Tyr Lys Gly Thr Trp Ser Phe Ile Thr Ala Ala Glu Asn
 175 180 185

FIG.3C.

GCC AAG AAT TAT GAA TTG TTA AGA AAT TCT GGT GCC GGT CAA GCT TAT
Gly Lys Asn Tyr Glu Leu Arg Asn Ser Gly Gly Gln Ala Tyr
190 195 200 205

TCT CGA CGT AGT GCT ACT CCA GAA GAT ATT GAT TTA GAT CGT AAG ACG
Ser Arg Arg Ser Ala Thr Pro Glu Asp Ile Asp Leu Asp Arg Lys Thr
210 215 220

GCC TTA ACA AGT GAA TTT ACT GTC AAT TTT GGT ACA AAA AAG CTC ACT
Gly Leu Thr Ser Glu Phe Thr Val Asn Phe Gly Thr Lys Lys Leu Thr
225 230 235

GGA GGA CTT TAT TAT AAT TTA CGT GAA ACA GAT GCT AAT AAA TCA CAA
Gly Gly Leu Tyr Tyr Asn Leu Arg Glu Thr Asp Ala Asn Lys Ser Gln
240 245 250

AAT AGA ACA CAT AAA CTC TAC GAT CTA GAA GCT GAT GTT CAT AGC AAC
Asn Arg Thr His Lys Leu Tyr Asp Leu Glu Ala Asp Val His Ser Asn
255 260 265

CGA TTC AGG GGT AAA GTA AAG CCA ACC AAA AAA GAG TCT TCT GAA GAA
Arg Phe Arg Gly Lys Val Lys Pro Thr Lys Lys Glu Ser Ser Glu Glu
270 275 280 285

FIG. 3D.

CAT CCC TTT ACC AGC GAG GGA ACA TTA GAA GGT GGT TTT TAC GGG CCT
 His Pro Phe Thr Ser Glu Gly Thr Leu Glu Gly Phe Tyr Gly Pro
 295 300

GAG GGT CAA GAA TTA GGA GGA AAG TTT TTA GCT CAC GAC AAA AAA GTT
 Glu Gly Gln Glu Phe Ser Ala Lys Phe Leu Ala His Asp Lys Lys Val
 305 310 315

TTC GGG GTA TTT AGT GCC AAA GAA CAG CAA GAA ACG TCA GAA AAC AAA
 Leu Gly Val Phe Ser Ala Lys Glu Gln Gln Glu Thr Ser Glu Asn Lys
 320 325 330

AAA TTA CCC AAA GAA ACC TTA ATT GAT GGC AAG CTA ACT ACT TTT AAA
 Lys Leu Pro Lys Glu Thr Leu Ile Asp Gly Lys Leu Thr Thr Phe Lys
 335 340 345

ACA ACC AAT GCA ACA GCC AAT GCA ACA ACC GAT GCA ACA ACC AGT ACA
 Thr Thr Asn Ala Thr Ala Asn Ala Thr Thr Asp Ala Thr Thr Ser Thr
 350 355 360 365

ACA GCC AGT ACA AAA ACC GAT ACA ACA ACC AAT GCA ACA GCC AAT ACA
 Thr Ala Ser Thr Lys Thr Asp Thr Thr Thr Asn Ala Thr Ala Asn Thr
 370 375 380

FIG. 3E.

GAA AAC TTT ACG ACA AAA GAT ATA CCA AGT TTG GGT GAA GCT GAT TAT
Glu Asn Phe Thr Thr Lys Asp Ile Pro Ser Leu Gly Glu Ala Asp Tyr
385 390

CTT TTA ATT GAT AAT TAC CCT GGT CTT TTC CCT GAG AGT GGT GAT
Leu Leu Ile Asp Asn Tyr Pro Val Pro Leu Phe Pro Glu Ser Gly Asp
400 405 410

TTC ATA AGT AGT AAG CAC CAT ACT GTA GGA AAG AAA ACC TAT CAA GTA
Phe Ile Ser Ser Lys His His Thr Val Gly Lys Lys Thr Tyr Gln Val
415 420 425

GAA GCA TGT TCC AGT AAT CTA ACC TAT GTA AAA TTT GGT ATG TAT TAT
Glu Ala Cys Cys Ser Asn Leu Ser Tyr Val Lys Phe Gly Met Tyr Tyr
430 435 440 445

GAA GCC CCA CCT AAA GAA GAA GAA AAA GAA AAA GAC AAA GAC
Glu Ala Pro Pro Lys Glu Glu Glu Lys Glu Lys Lys Asp Lys Asp
450 455 460

AAA GAA AAA GAA AAA CAA GCG ACA ACA TCT ATC AAG ACT TAT TAT CAA
Lys Glu Lys Lys Lys Gln Ala Thr Thr Ser Ile Lys Thr Tyr Tyr Gln
465 470 475

FIG. 3F.

TTC TTA TTA GGT CTC GGT ACT CCC AGT TCT GAA ATA CCT AAA GAA GGA
 Phe Leu Leu Gly Leu Arg Thr Pro Ser Ser Glu Ile Pro Lys Glu Gly
 480 485 490
 AGT GCA AAA TAT CAT GGT AAT TCG TTT GGT TAT ATT AGT GAT GGC GAG
 Ser Ala Lys Tyr His Gly Asn Trp Phe Gly Tyr Ile Ser Asp Gly Glu
 495 500 505
 ACA TCT TAC TCC GCC AGT GGT GAT AAG GAA CCC AGT AAA AAT GCT GTC
 Thr Ser Tyr Ser Ala Ser Gly Asp Lys Glu Arg Ser Lys Asn Ala Val
 510 520 525
 GCC GAG TTT AAT GTA AAT TTT GCC GAG AAA ACA TTA ACA GGC GAA TTA
 Ala Glu Phe Asn Val Asn Phe Ala Glu Lys Thr Leu Thr Gly Glu Leu
 530 535 540
 AAA CGA CAC GAT ACT CAA AAT CCC GTA TTT AAA ATT AAT GCA ACC TTT
 Lys Arg His Asp Thr Gln Asn Pro Val Phe Lys Ile Asn Ala Thr Phe
 545 550 555
 CAA AGT GGT AAG AAT GAC TTC ACT GGT ACA GCA ACC GCA AAA GAT TTA
 Gln Ser Gly Lys Asn Asp Phe Thr Gly Thr Ala Thr Ala Lys Asp Leu
 560 565 570

FIG.36.

GCA ATA GAT GGT AAA AAT ACA CAA GGC ACA TCT AAA GTC AAT TTC ACG
Ala Ile Asp Gly Lys Asn Thr Gln Gly Thr Ser Lys Val Asn Phe Thr
575 585

GCA ACA GTA AAC GGG GCA TTT TAT GGT CCG CAC GCT ACA GAA TTA GGC
Ala Thr Val Asn Gly Ala Phe Tyr Gly Pro His Ala Thr Glu Leu Gly
590 595 600 605

GGT TAT TTC ACC TAT AAC GGA AAC AAT CCT ACA GAT AAA AAT TCA TCA
Gly Tyr Phe Thr Tyr Asn Gly Asn Asn Pro Thr Asp Lys Asn Ser Ser
610 615 620

TCC AAT TCA GAA AAG GCA AGA GCT GCC GAT GTG TTT GGA GCT AAA AAA
Ser Asn Ser Glu Lys Ala Arg Ala Val Phe Gly Ala Lys Lys
625 630 635

CAA CAA GTA GAA ACA ACC AA GFAATGGAAT ACTAAA A ATG ACT AAA AAA
Gln Gln Val Glu Thr Thr Lys Met Thr Lys Lys
640 645

CCC TAT TTT CGC CTA AGT ATT ATT TCT TGT CTT TTA ATT TCA TGC TAT
Pro Tyr Phe Arg Leu Ser Ile Ile Ser Cys Leu Ile Ser Cys Tyr
650 655 660

FIG.3H.

GTA AAA GCA GAA ACT CAA AGT ATA AAA GAT ACA AAA GAA GCT ATA TCA
 Val Lys Ala Glu Thr Gln Ser Ile Lys Asp Thr Lys Glu Ala Ile Ser
 665 670 675 680
 TCT GAA GTG GAC ACT CAA AGT ACA GAA GAT TCA GAA TTA GAA ACT ATC
 Ser Glu Val Asp Thr Gln Ser Thr Glu Asp Ser Glu Leu Glu Thr Ile
 685 690 695
 TCA GTC ACT GCA GAA AAA GTT ACA GAT CGT AAA GAT AAT GAA GTA ACT
 Ser Val Thr Ala Glu Lys Val Arg Asp Arg Lys Asp Asn Glu Val Thr
 700 705 710
 CGA CTT GGC AAA ATT ATA AAA ACT AGT GAA AGT ATC AGC CGA GAA CAA
 Gly Leu Gly Lys Ile Ile Lys Thr Ser Glu Ser Ile Ser Arg Glu Gln
 715 720 725
 GTA TTA AAT ATT CGT GAT CTA ACA CGC TAT GAT CCA GCG ATT TCA GTT
 Val Leu Asn Ile Arg Asp Leu Thr Arg Tyr Asp Pro Gly Ile Ser Val
 730 735 740
 GTA GAA CAA GGT CGC GGT GCA AGT TCT GCA TAT TCT ATT CGT GGT ATG
 Val Glu Gln Gly Arg Gly Ala Ser Ser Gly Tyr Ser Ile Arg Gly Met
 745 750 755 760

FIG.31.

CAC ACA AAT ACA GTT GCT TTA GTA GAT GGT TTA CCT CAA ACG CAA
 Asp Arg Asn Arg Val Ala Leu Val Asp Gly Leu Pro Gln Thr Gln
 765 770 775
 TCT TAT GTA GTG CAA AGC CCT TTA GTT CCT CGT TCA GGA TAT TCT GGC
 Ser Tyr Val Val Gln Ser Pro Leu Val Ala Arg Ser Gly Tyr Ser Gly
 780 785 790
 ACT GGT GCA ATT AAT CAA ATT GAA TAT GAA AAT GTA AAG GCC GTC GAA
 Thr Gly Ala Ile Asn Glu Ile Glu Tyr Glu Asn Val Lys Ala Val Glu
 795 800 805
 ATA AGC AAG GGG GGG AGT TCT TCT GAG TAT GGT AAT GGA GCA CTA GCT
 Ile Ser Lys Gly Gly Ser Ser Glu Tyr Gly Asn Gly Ala Leu Ala
 810 815 820
 GGT TCT GTA ACA TTT CAA AGC AAA TCA GCA GCC GAT ATC TTA GAA GGA
 Gly Ser Val Thr Phe Gln Ser Lys Ser Ala Ala Asp Ile Leu Glu Gly
 825 830 835 840
 GAC AAA TCA TGG GGA ATT CAA ACT AAA AAT GCT TAT TCA AGC AAA AAT
 Asp Lys Ser Trp Gly Ile Gln Thr Lys Asn Ala Tyr Ser Ser Lys Asn
 845 850 855

FIG.3 J.

AAA GGC TTT ACC CAT TCT TTA GCT GTA GGA AAA CAA GGT GGA TTT
 Lys Gly Phe Thr His Ser Leu Ala Val Ala Gly Lys Gln Gly Gly Phe
 860 865
 GAA GGG GTC GGC ATT TAC ACT CAC CGA AAT TCA ATT GAA ACC CAA GTC
 Glu Gly Val Ala Ile Tyr Thr His Arg Asn Ser Ile Glu Thr Gln Val
 875 880 885
 CAT AAA GAT GCA TTA AAA GGC GTG CAA AGT TAT GAT CGA TTC ATC GCC
 His Lys Asp Ala Leu Lys Gly Val Gln Ser Tyr Asp Arg Phe Ile Ala
 890 895
 ACA ACA GAG GAT CAA TCT GCA TAC TTT GTG ATG CAA GAT GAG TGT CTA
 Thr Thr Glu Asp Gln Ser Ala Tyr Phe Val Met Gln Asp Glu Cys Leu
 905 910 915
 GAT GGT TAT GAC AAG TGT AAA ACT TCA CCC AAA CGA CCT GCG ACT TTA
 Asp Gly Tyr Asp Lys Cys Lys Thr Ser Pro Lys Arg Pro Ala Thr Leu
 920 930 935
 TCC ACC CAA AGA GAA ACC GTA AGC GTT TCA GAT TAT ACG GGG GCT AAC
 Ser Thr Gln Arg Glu Thr Val Ser Val Ser Asp Tyr Thr Gly Ala Asn
 940 945 950

FIG.3K.

CGT ATC AAA CCT AAT CCA ATG AAA TAT GAA AGC CAG TCT TGG TTT TTA
 Arg Ile Lys Pro Asn Pro Met Lys Tyr Glu Ser Trp Phe Leu
 955 960 965

AGA GGA GGT TAT CAT TTT TCT GAA CAA CAC TAT ATT GGT GGT ATT TTT
 Arg Gly Gly Tyr His Phe Ser Glu Gln His Tyr Ile Gly Ile Phe
 970 975 980

GAA TTC ACA CAA CAA AAA TTT GAT ATC GGT GAT ATG ACA TTT CCC GCT
 Glu Phe Thr Gln Gln Lys Phe Asp Ile Arg Asp Met Thr Phe Pro Ala
 985 990 995 1000

TAT TTA AGG CCA ACA GAA GAC AAG GAT TTA CAA AGT CCC CCT TTT TAT
 Tyr Leu Arg Pro Thr Glu Asp Lys Asp Leu Gln Ser Arg Pro Phe Tyr
 1005 1010 1015

CCA AAG CAA GAT TAT GGT GCA TAT CAA CAT ATT GGT GAT GGC AGA GGC
 Pro Lys Gln Asp Tyr Gly Ala Tyr Gln His Ile Gly Asp Gly Arg Gly
 1020 1025 1030

GTT AAA TAT GCA AGT GGG CTT TAT TTC CAT GAA CAC CAT AGA AAA CAG
 Val Lys Tyr Ala Ser Gly Leu Tyr Phe Asp Glu His His Arg Lys Gln
 1035 1040 1045

FIG.3L.

CGT GTA GGT ATT GAA TAT ATT TAC GAA AAT AAG AAC AAA GCG GCG ATC
Arg Val Gly Ile Glu Tyr Ile Tyr Glu Asn Lys Asn Lys Ala Gly Ile
1050 1055 1060

ATT GAC AAA GCG GTG TTA AGT GCT AAT CAA ACA TCA TAC TTG ACA
Ile Asp Lys Ala Val Leu Ser Ala Asn Gln Thr Ser Tyr Leu Thr
1065 1070 1075 1080

GTT ATA TGC GAC ATA GCG ATT GCA GTC TTT ATC CAT AAT CCA AGT AAG
Val Ile Cys Asp Ile Arg Ile Ala Val Phe Ile His Asn Pro Ser Lys
1085 1090 1095

AAT TGC GCG CCA ACA CTT GAT AAA CCT TAT TCA TAC TAT CAT TCT GAT
Asn Cys Arg Pro Thr Leu Asp Lys Pro Tyr Ser Tyr His Ser Asp
1100 1105 1110

ACA AAT GTT TAT AAA GAA AAA CAT AAC ATG TTG CAA TTG AAT TTA GAG
Arg Asn Val Tyr Lys Glu Lys His Asn Met Leu Gln Leu Asn Leu Glu
1115 1120 1125

AAA AAA ATT CAA CAA AAT TGG CTT ACT CAT CAA ATT GCG TTC AAT CTT
Lys Lys Ile Gln Gln Asn Thr Leu Thr His Gln Ile Ala Phe Asn Leu
1130 1135 1140

FIG. 3 M.

GGT TTT GAT GAC TTT ACT TCC GCA CTT CAG CAT AAA GAT TAT TTA ACT
 Gly Phe Asp Asp Phe Thr Ser Ala Leu Gln His Lys Asp Tyr Leu Thr 1160
 1145 1150 1155

CGA CGT GTT ATC GCT AGG GCA AGT AGT ATT TCA GAG AAA CGT GGT GAA
 Arg Arg Val Ile Ala Thr Ala Ser Ser Ile Ser Glu Lys Arg Gly Glu 1175
 1165 1170

GCA AGA AGA AAT GGT TTA CAA TCA AGT CCT TAC TTA TAC CCA ACA CCA
 Ala Arg Arg Asn Gly Leu Gln Ser Ser Pro Tyr Leu Tyr Pro Thr Pro 1190
 1180 1185

AAA GCA GAG TTG GTA GGA GAT CTT TGT AAT TAT CAA GGT AAG TCC
 Lys Ala Glu Leu Val Gly Gly Asp Leu Cys Asn Tyr Gln Gly Lys Ser 1205
 1195 1200

TCT AAT TAC AGT GAC TGT AAA GTG CCG TTA ATT AAA GGG AAA AAT TAT
 Ser Asn Tyr Ser Asp Cys Lys Val Arg Leu Ile Lys Gly Lys Asn Tyr 1220
 1210 1215

TAT TTC GCA GCA CCG AAT AAT ATG GCA TTA GGG AAA TAC GTT GAT TTA
 Tyr Phe Ala Ala Arg Asn Asn Met Ala Leu Gly Lys Tyr Val Asp Leu 1240
 1225 1230 1235

FIG.3N.

GGT TTA GGT ATG AGG TAT GAC GTA TCT CGT ACA AAA GCT AAT GAA TCA
Gly Leu Gly Met Arg Tyr Asp Val Ser Arg Thr Lys Ala Asn Glu Ser
1245 1250 1255

ACT ATT AGT GTT GGT AAA TTT AAA AAT TTC TCT TGG AAT ACT GGT ATT
Thr Ile Ser Val Gly Lys Phe Lys Asn Phe Ser Trp Asn Thr Gly Ile
1260 1265 1270

GTC ATA AAA CCA ACG GAA TGG CTT GAT CTT TCT TAT CGC CTT TCT ACT
Val Ile Lys Pro Thr Glu Trp Leu Asp Leu Ser Tyr Arg Leu Ser Thr
1275 1280 1285

GGA TTT ACA AAT CCT AGT TTT GCT GAA ATG TAT GGT TGG CGG TAT GGT
Gly Phe Arg Asn Pro Ser Phe Ala Glu Met Tyr Gly Trp Arg Tyr Gly
1290 1295 1300

GGC AAG GAT ACC GAT GTT TAT ATA GGT AAA TTT AAG CCT GAA ACA TCT
Gly Lys Asp Thr Asp Val Tyr Ile Gly Lys Phe Lys Pro Glu Thr Ser
1305 1310 1315 1320

GGT AAC CAA GAG TTT GGT CTC GCT CTA AAA GGG GAT TTT GGT AAT ATT
Arg Asn Gln Glu Phe Gly Leu Ala Leu Lys Gly Asp Phe Gly Asn Ile
1325 1330 1335

FIG.30.

GAG ATC AGT CAT TTT AGT AAT GCT TAT CGA AAT CTT ATC GCC TTT GCT
 Glu Ile Ser His Phe Ser Asn Ala Tyr Arg Asn Leu Ile Ala Phe Ala
 1340 1345

GAA CAA CTT AGT AAA AAT CGA ACT ACT GGA AAG GCC AAT TAT CGA TAT
 Glu Glu Leu Ser Lys Asn Gly Thr Thr Gly Lys Gly Asn Tyr Gly Tyr
 1355 1360 1365

CAT AAT GCA CAA AAT CCA AAA TTA GTT GGC GTA AAT ATA ACT GCG CAA
 His Asn Ala Gln Asn Ala Lys Leu Val Gly Val Asn Ile Thr Ala Gln
 1370 1375 1380

TTA GAT TTT AAT GGT TTA TCG AAA CGT ATT OCC TAC GGT TGG TAT GCA
 Leu Asp Phe Asn Gly Leu Trp Lys Arg Ile Pro Tyr Gly Trp Tyr Ala
 1385 1390 1395 1400

ACA TTT GCT TAT AAC CGA GTA AAA GTT AAA GAT CAA AAA ATC AAT GCT
 Thr Phe Ala Tyr Asn Arg Val Lys Val Lys Asp Gln Lys Ile Asn Ala
 1405 1410 1415

GGT TTA GCT TCC GTA AGC AGT TAT TTA TTT GAT GCC ATT CAG OCC AGC
 Gly Leu Ala Ser Val Ser Ser Tyr Leu Phe Asp Ala Ile Gln Pro Ser
 1420 1425 1430

FIG.3P.

CGT TAT ATC ATT GGT TTA GCG TAT GAT CAT CCA AGT AAT ACT TCG CGA
Arg Tyr Ile Ile Gly Leu Gly Tyr Asp His Pro Ser Asn Thr Trp Gly
1435 1440 1445

ATT AAG ACA ATG TTT ACT CAA TCA AAA GCA AAA TCT CAA AAT GAA TTG
Ile Lys Thr Met Phe Thr Gln Ser Lys Ala Lys Ser Gln Asn Glu Leu
1450 1455 1460

CTA GCA AAA CGT GCA TTG GGT AAC AAT TCA AGG AAT GTA AAA TCA ACA
Leu Gly Lys Arg Ala Leu Gly Asn Asn Ser Arg Asn Val Lys Ser Thr
1465 1470 1475 1480

AGA AAA CTT ACT CCG GCA TCG CAT ATC TTA GAT GTA TCG GGT TAT TAC
Arg Lys Leu Thr Arg Ala Trp His Ile Leu Asp Val Ser Gly Tyr Tyr
1485 1490 1495

ATG GTG AAT AGA AGT ATT TTG TTC CCA TTA GCA GTA TAT AAT TTA TTA
Met Val Asn Arg Ser Ile Leu Phe Arg Leu Gly Val Tyr Asn Leu Leu
1500 1505 1510

AAC TAT CCG TAT GTC ACT TCG GAA GCG GTG CGT CAA ACA GCA CAA GGT
Asn Tyr Arg Tyr Val Thr Trp Glu Ala Val Arg Gln Thr Ala Gln Gly
1515 1520 1525

FIG.3Q.

GCG GTC AAT CAA CAT CAA AAT GTT GGT AAC TAT ACT CCG TAC GCA GCA
 Ala Val Asn Gln His Gln Asn Val Gly Asn Tyr Thr Arg Tyr Ala Ala
 1530 1540

TCA GCA CGA AAC TAT ACC TTA ACA TTA GAA ATG AAA TTC TAA
 Ser Gly Arg Asn Tyr Thr Leu Thr Leu Glu Met Lys Phe
 1545 1550 1555

FIG. 4 A.

GCACAGCTA CATTGGTTAA TGAATAGCCT ATAAATGATA AGAAGAAAT TTGTTTACG

CCATTITTCATTTTATCC ATGAACTTAA AAAACTCTAA CTTCACATTA TTACAAAAA
⁻³⁵

AGATCAATTA⁻¹⁰ TGGCAATTAT TATCAATTAT^{RBS} GTATGAGTAT ATAAATCT AUG AAA TCT
 Met Lys Ser
 1

GTA CCT CTT ATC TCT GGT GGA CTT TCC TTT TTA CTA AGT GCT TGT AGC
 Val Pro Leu Ile Ser Gly Gly Leu Ser Phe Leu Leu Ser Ala Cys Ser
 5 10 15

GGA GGG GGG TCT TTT GAT GTA GAT AAC GTC TCT AAT ACC CCC TCT TCT
 Gly Gly Gly Ser Phe Asp Val Asp Asn Val Ser Asn Thr Pro Ser Ser
 20 25 30 35

AAA CCA CGT TAT CAA GAC GAT ACC TCG AAT CAA AGA AAA AAA TCT AAT
 Lys Pro Arg Tyr Gln Asp Asp Thr Ser Asn Gln Arg Lys Lys Ser Asn
 40 45 50

TTG AAA AAG TTG TTC ATT CCT TCT TTA GGA GCG ATG AAA TTG GTG
 Leu Lys Lys Leu Phe Ile Pro Ser Leu Gly Gly Met Lys Leu Val
 55 60 65

FIG. 4B.

GCT CAG AAT CTT CGT GGT ANT AAA GAA CCT AGT TTC TTA AAT GAA GAT
 Ala Gln Asn Leu Arg Gly Asn Lys Glu Pro Ser Phe Leu Asn Glu Asp
 70 75
 GAC TAT ATA TCA TAT TTT TCC TCA CTT TCT ACG ATT GAA AAG GAT GTT
 Asp Tyr Ile Ser Tyr Phe Ser Ser Leu Ser Thr Ile Glu Lys Asp Val
 85 90 95
 AAA GAT AAC AAT AAA AAC GCG GCG GAC CTT ATT GCG TCA ATA GAC GAG
 Lys Asp Asn Asn Lys Asn Gly Ala Asp Leu Ile Gly Ser Ile Asp Glu
 100 105 110 115
 OCT AGT ACA ACA AAT CCA CCC GAA AAG CAT CAT GGA CAA AAA TAT GTA
 Pro Ser Thr Thr Asn Pro Pro Glu Lys His His Gly Gln Lys Tyr Val
 120 125 130
 TAT TCA GCG CTT TAT TAT ACT CCA TCG TGG AGT TTA AAC GAT TCT AAA
 Tyr Ser Gly Leu Tyr Tyr Thr Pro Ser Trp Ser Leu Asn Asp Ser Lys
 135 140 145
 AAC AAG TTT TAT TTA GGT TAC TAT GGA TAT GCG TTT TAT TAT GGT AAT
 Asn Lys Phe Tyr Leu Gly Tyr Tyr Gly Tyr Ala Phe Tyr Tyr Gly Asn
 150 155 160

FIG. 4C.

AAA ACT CCA ACA AAC TTG CCA GTA AAC GGT GTA OCT AAA TAC AAA GGA	165	170	175
Lys Thr Ala Thr Asn Leu Pro Val Asn Gly Val Ala Lys Tyr Lys Gly			
ACT TGG GAT TTC ATC ACT CCA ACT AAA AAT GCG AAA CGT TAT CCT TTG	180	185	190
Thr Trp Asp Phe Ile Thr Ala Thr Lys Asn Gly Lys Arg Tyr Pro Leu			195
TTA AGT AAT GCG AGT CAC GCT TAT TAT CGA CGT AGT GCA ATT CCA GAA	200	205	210
Leu Ser Asn Gly Ser His Ala Tyr Tyr Arg Arg Ser Ala Ile Pro Glu			
GAT ATT GAT TTA GAA AAT GAT TCA AAG AAT GGT GAT ATA GCG TTA ATA	215	220	225
Asp Ile Asp Leu Glu Asn Asp Ser Lys Asn Gly Asp Ile Gly Leu Ile			
AGT GAA TTT AGT CCA GAT TTT GGG ACT AAA AAA CTG ACA GGA CAA CTG	230	235	240
Ser Glu Phe Ser Ala Asp Phe Gly Thr Lys Lys Leu Thr Gly Gln Leu			
TCT TAC ACC AAA AGA AAA ACT AAT AAT CAA CCA TAT GAA AAG AAA AAA	245	250	255
Ser Tyr Thr Lys Arg Lys Thr Asn Asn Gln Pro Tyr Glu Lys Lys Lys			

FIG.4D.

CTC TAT GAT ATA GAT GCC GAT ATT TAT AGT AAT AGA TTC AGG GGT ACA
 Leu Tyr Asp Ile Asp Ala Asp Ile Tyr Ser Asn Arg Phe Arg Gly Thr 275
 260

GTA AAG CCA ACC GAA AAA GAT TCT GAA GAA CAT OCC TTT ACC AGC GAG
 Val Lys Pro Thr Leu Lys Asp Ser Glu Glu His Pro Phe Thr Ser Glu 290
 280

CGA ACA TTA GAA GGT GGT TTT TAT GGG CCT AAT GCT GAA GAA CTA GGG
 Gly Thr Leu Glu Gly Gly Phe Tyr Gly Pro Asn Ala Glu Leu Gly 305
 295

GGG AAA TTT TTA GCT ACG GAT AAC CGA GTT TTT GGG GTA TTT AGT GCC
 Gly Lys Phe Leu Ala Thr Asp Asn Arg Val Phe Gly Val Phe Ser Ala 320
 310

AAA GAA ACG GAA GAA ACA AAA AAG GAA GCG TTA TCC AAG GAA ACC TTA
 Lys Glu Thr Glu Glu Thr Lys Lys Glu Ala Leu Ser Lys Glu Thr Leu 335
 325

ATT GAT GCC AAG CTA ATT ACT TTC TCT ACT AAA AAA ACC GAT GCA AAA
 Ile Asp Gly Lys Leu Ile Thr Phe Ser Thr Lys Lys Thr Asp Ala Lys 355
 340

FIG.4E.

ACC AAT GCA ACA ACC AGT ACC GCA GCT AAT ACA ACA ACC GAT ACA ACC
 Thr Asn Ala Thr Ser Thr Ala Ala Asn Thr Thr Asp Thr Thr 370
 360

GCC AAT ACA ATA ACC GAT GAA AAA AAC TTT AAG ACG GAA GAT ATA TCA
 Ala Asn Thr Ile Thr Asp Glu Lys Asn Phe Lys Thr Glu Asp Ile Ser 385
 375 380

AGT TTT GGT GAA GCT GAT TAT CTG TTA ATT GAC AAA TAT CCT ATT CCA
 Ser Phe Gly Glu Ala Asp Tyr Leu Leu Ile Asp Lys Tyr Pro Ile Pro 400
 390 395

CTT TTA CCT GAT AAA AAT ACT AAT GAT TTC ATA AGT AGT AAG CAT CAT
 Leu Leu Pro Asp Lys Asn Thr Asn Asp Phe Ile Ser Ser Lys His His 415
 405 410

ACT GTA GGA AAT AAA GCG TAT AAA GTG GAA GCA TGT TGC AGT AAT CTA
 Thr Val Gly Asn Lys Arg Tyr Lys Val Glu Ala Cys Ser Asn Leu 435
 420 425 430

ACC TAT GTG AAA TTT GGT ATG TAT TAT GAA GAC CCA CTT AAA GAA AAA
 Ser Tyr Val Lys Phe Gly Met Tyr Tyr Glu Asp Pro Leu Lys Glu Lys 450
 440 445 450

FIG. 4F.

GAA ACA GAA ACA GAA ACA GAA AAA GAC AAA GAA AAA GAA AAA
 Glu Thr Glu Thr Glu Thr Glu Thr Lys Asp Lys Glu Lys Glu Lys
 455 460 465

GAA AAA GAC AAA GAC AAA GAA CAA AAG GCG GCA ACG ACC AAC ACT
 Glu Lys Asp Lys Asp Lys Glu Lys Gln Thr Ala Ala Thr Thr Asn Thr
 470 475 480

TAT TAT CAA TTC TTA TTA GGT CAC CGT ACT CCC AAG GAC GAC ATA CCT
 Tyr Tyr Gln Phe Leu Leu Gly His Arg Thr Pro Lys Asp Asp Ile Pro
 485 490 495

AAA ACA GGA AGT GCA AAA TAT CAT GGT AGT TGG TTT GGT TAT ATT ACT
 Lys Thr Gly Ser Ala Lys Tyr His Gly Ser Trp Phe Gly Tyr Ile Thr
 500 505 510 515

GAC GGT AAG ACA TCT TAC TCC CCC AGT GGT GAT AAG AAA CCG GAT AAA
 Asp Gly Lys Thr Tyr Ser Pro Ser Gly Asp Lys Lys Arg Asp Lys
 520 525 530

AAT GGT GTC GCC GAG TTT AAT GTT GAT TTT GCC GAG AAA AAG CTA ACA
 Asn Ala Val Ala Glu Phe Asn Val Asp Phe Ala Glu Lys Lys Leu Thr
 535 540 545

FIG.46.

GCC GAA TTA AAA CCA CAC GAT ACT GGA AAT CCC GTA TTT AGT ATT GAG
 Gly Glu Leu Lys Arg His Asp Thr Gly Asn Pro Val Phe Ser Ile Glu
 550 555

GCA AAC TTT AAT AAT AGT AGT AAT GCC TTC ACT GGT ACA GCA ACC GCA
 Ala Asn Phe Asn Asn Ser Ser Asn Ala Phe Thr Gly Thr Ala Thr Ala
 565 570 575

ACA AAT TTT GTA ATA GAT GGT AAA AAT AGT CAA AAT AAA AAT ACC CCA
 Thr Asn Phe Val Ile Asp Gly Lys Asn Ser Gln Asn Lys Asn Thr Pro
 580 585 590 595

ATT AAT ATT ACA ACT AAA GTA AAC GGG GCA TTT TAT GGA CCT AAG GCT
 Ile Asn Ile Thr Thr Lys Val Asn Gly Ala Phe Tyr Gly Pro Lys Ala
 600 605 610

TCT GAA TTA GGC GGT TAT TTC ACT TAT AAC GGA AAT TCT ACA GCT ACA
 Ser Glu Leu Gly Gly Tyr Phe Thr Tyr Asn Gly Asn Ser Thr Ala Thr
 615 620 625

AAT TCT GAA AGT TCC TCA ACC GTA TCT TCA TCA TCC AAT TCA AAA AAT
 Asn Ser Glu Ser Ser Thr Val Ser Ser Ser Asn Ser Lys Asn
 630 635 640

FIG.4H.

GCA AGA GGT GCA GTT GTC TTT GGT GCG AGA CAA CAA GTA GAA ACA ACC
 Ala Arg Ala Ala Val Phe Gly Ala Arg Gln Val Glu Thr Thr
 645 650 655

AAA TATGGAAATA CTA AAA ATG ACT AAA CCC TAT TTT CGC CTA AGT
 Lys Met Thr Lys Lys Pro Tyr Phe Arg Leu Ser
 660 665 670

ATT ATT TCT TGT CTT TTA ATT TCA TGC TAT GTA AAA CCA ACT CAA
 Ile Ile Ser Cys Leu Leu Ile Ser Cys Tyr Val Lys Ala Glu Thr Gln
 675 680 685

AGT ATA AAA GAT ACA AAA GAA GCT ATA TCA TCT GAA GTG GAC ACT CAA
 Ser Ile Lys Asp Thr Lys Glu Ala Ile Ser Ser Glu Val Asp Thr Gln
 690 695 700

AGT ACA GAA GAT TCA GAA TTA GAA ACT ATC TCA GTC ACT CCA GAA AAA
 Ser Thr Glu Asp Ser Glu Leu Glu Thr Ile Ser Val Thr Ala Glu Lys
 705 710 715

ATA ACA GAT CGT AAA GAT AAT GAA GTA ACT GCA CTT GGC AAA ATT ATC
 Ile Arg Asp Arg Lys Asp Asn Glu Val Thr Gly Leu Gly Lys Ile Ile
 720 730 735

FIG.41.

AAA ACT AGT GAA AGT ATC AGC CGA CAA GTA TTA AAT ATT CGT GAT
 Lys Thr Ser Glu Ser Ile Ser Arg Glu Gln Val Leu Asn Ile Arg Asp 735
 740 745 750
 CTA ACA CGC TAT GAT CCA CGG ATT TCA GTT GTA GAA CAA GGT CGC GGT
 Leu Thr Arg Tyr Asp Pro Gly Ile Ser Val Val Glu Gln Gly Arg Gly 755
 760 765
 GCA AGT TCT GGA TAT TCT ATT CGT GGT ATG GAC AGA AAT AGA GTT GCT
 Ala Ser Ser Gly Tyr Ser Ile Arg Gly Met Asp Arg Asn Arg Val Ala 770
 775 780
 TTA TTA GTA GAT GGT TTA CCT CAA ACG CAA TCT TAT GTA GTG CAA ACG
 Leu Leu Val Asp Gly Leu Pro Gln Thr Gln Ser Tyr Val Val Gln Ser 785
 790 795
 OCT TTA GTT GCT GGT TCA GGA TAT TCT CGC ACT CGT GCA ATT AAT GAA
 Pro Leu Val Ala Arg Ser Gly Tyr Ser Gly Thr Gly Ala Ile Asn Glu 800
 805 810
 AAT GAA TAT GAA AAT GTA AAG GCC GTC GAA ATA ACG AAG CGG GCG AGT
 Ile Glu Tyr Glu Asn Val Lys Ala Val Glu Ile Ser Lys Gly Gly Ser 815
 820 825 830

FIG.4J.

TCT TCT CAG TAT GGT AAT GGA CTA GCT GGT TCT GTA ACA TTT CAA	
Ser Ser Glu Tyr Gly Asn Gly Ala Leu Ala Gly Ser Val Thr Phe Gln	845
	835 . 840
AGC AAA TCA GCA GCC GAT ATC TTA GAA GGA GAC AAA TCA TGG GGA ATT	
Ser Lys Ser Ala Ala Asp Ile Leu Glu Gly Asp Lys Ser Trp Gly Ile	860
	855
CAA ACT AAA AAT GCT TAT TCA AGC AAA AAT AAA GGC TTT ACC CAT TCT	
Gln Thr Lys Asn Ala Tyr Ser Ser Lys Asn Lys Gly Phe Thr His Ser	875
	865 870
TTA GGT GTA GCA GGA AAA CAA GGT GGA TTT GAA GGG CTA GCC ATT TAC	
Leu Ala Val Ala Gly Lys Gln Gly Gly Phe Glu Gly Leu Ala Ile Tyr	885
	880
ACT CAA CGA AAT TCA ATT GAA ACC CAA GTC CAT AAA GAT GCA TTA AAA	
Thr Gln Arg Asn Ser Ile Glu Thr Gln Val His Lys Asp Ala Leu Lys	910
	895 900 905
GGC GTA CAA AGT TAT GAT CGA TTA ATC GCC ACA ACA GAT AAA TCT TCA	
Gly Val Gln Ser Tyr Asp Arg Leu Ile Ala Thr Thr Asp Lys Ser Ser	925
	915 920

FIG. 4K.

GCA TAC TTT GTG ATA CAA GGT GAG TGT CCA AAT GGT GAT GAC AAG TGT
Gly Tyr Phe Val Ile Gln Gly Glu Cys Pro Asn Gly Asp Asp Lys Cys
930 935

GCA GCC AAG CCA CCT GGG ACT TTA TCC ACC CAA AGC GAA ACC GTA AGC
Ala Ala Lys Pro Pro Ala Thr Leu Ser Thr Gln Ser Glu Thr Val Ser
940 945

GTT TCA GAT TAT ACG GGG GCT AAC GGT ATC AAA OCT AAT CCA ATG AAA
Val Ser Asp Tyr Thr Gly Ala Asn Arg Ile Lys Pro Asn Pro Met Lys
950 955

TAT GAA AGC CAG TCT TGG TTT TTA AGA GGA GGT TAT CAT TTT TCT GAA
Tyr Glu Ser Gln Ser Trp Phe Leu Arg Gly Tyr His Phe Ser Glu
960 965

CAA CAT TAT ATT GGT GGT ATT TTT GAA TTC ACA CAA AAA TTT GAT
Gln His Tyr Ile Gly Gly Ile Phe Glu Phe Thr Gln Gln Lys Phe Asp
970 975

ATC CGT GAT ATG ACA TTT CCC GCT TAT TTA AGC CCA ACA GAA AGA CGG
Ile Arg Asp Met Thr Phe Pro Ala Tyr Leu Ser Pro Thr Glu Arg Arg
980 985

1000 1005
1010 1015 1020

FIG.4L.

GAT GAT AGT AGT CQT TCT TTT TAT CCA ATG CAA GAT CAT GGT GCA TAT
 Asp Asp Ser Ser Arg Ser Phe Tyr Pro Met Gln Asp His Gly Ala Tyr
 1025 1030 1035

CAA CAT ATT GAG GAT GGC AGA GGC GTT AAA TAT GCA AGT GCG CTT TAT
 Gln His Ile Glu Asp Gly Arg Gly Val Lys Tyr Ala Ser Gly Leu Tyr
 1040 1045 1050

TTC GAT GAA CAC CAT AGA AAA CAG CGT GTA GGT ATT GAA TAT ATT TAC
 Phe Asp Glu His His Arg Lys Gln Arg Val Gly Ile Glu Tyr Ile Tyr
 1055 1060 1065 1070

GAA AAT AAG AAC AAA GCG GGC ATC ATT GAC AAA GCA GTG TTA AGT GCT
 Glu Asn Lys Asn Lys Ala Gly Ile Ile Asp Lys Ala Val Leu Ser Ala
 1075 1080 1085

AAT CAA CAA AAC ATC ATA CTT GAC AGT TAT ATG CCA CAT ACG CAT TGC
 Asn Gln Gln Asn Ile Ile Leu Asp Ser Tyr Met Arg His Thr His Cys
 1090 1095 1100

AGT CTT TAT CTT AAT CCA AGT AAG AAT TGC GCG CCA ACA CTT GAT AAA
 Ser Leu Tyr Pro Asn Pro Ser Lys Asn Cys Arg Pro Thr Leu Asp Lys
 1105 1110 1115

FIG.4M.

OCT TAT TCA TAC TAT GGT TCT GAT AGA AAT GTT TAT AAA GAA AAA CAT
Pro Tyr Ser Tyr Arg Ser Asp Arg Asn Val Tyr Lys Glu Lys His
1120 1125 1130

AAT ATG TTG CAA TTG AAT TTA GAG AAA AAA AAT CAA CAA AAT TGG CTT
Asn Met Leu Gln Leu Asn Leu Glu Lys Lys Ile Gln Gln Asn Trp Leu
1135 1140 1145 1150

ACT CAT CAA AAT GTC TTC AAT CTT GGT TTT GAT GAC TTT ACT TCA CCG
Thr His Gln Ile Val Phe Asn Leu Gly Phe Asp Asp Phe Thr Ser Ala
1155 1160 1165

CIT CAG CAT AAA GAT TAT TTA ACT CGA GGT GTT ATC GCT ACG GCA GAT
Leu Gln His Lys Asp Tyr Leu Thr Arg Arg Val Ile Ala Thr Ala Asp
1170 1175 1180

AGT ATT CCA AGG AAA CCT GGT GAA ACT GGT AAA CCA AGA AAT GGT TTG
Ser Ile Pro Arg Lys Pro Gly Glu Thr Gly Lys Pro Arg Asn Gly Leu
1185 1190 1195

CAA TCA CAA CCT TAC TTA TAC CCA AAA CCA GAG CCA TAT TTT CCA GGA
Gln Ser Gln Pro Tyr Leu Tyr Pro Lys Pro Glu Pro Tyr Phe Ala Gly
1200 1205 1210

FIG.4N.

CAA GAT CAT TGT AAT TAT CAA GGT AGC TCC TCT AAT TAC AGA GAC TGT
 Gln Asp His Cys Asn Tyr Gln Gly Ser Ser Asn Tyr Arg Asp Cys
 1215 1220 1225 1230
 AAA GTG CCG TTA ATT AAA CCG AAA AAT TAT TAT TTC GCA GCA CCG AAT
 Lys Val Arg Leu Ile Lys Gly Lys Asn Tyr Tyr Phe Ala Ala Arg Asn
 1235 1240 1245
 AAT ATG GCA TTA CCG AAA TAC GTT GAT TTA GGT TTA GGT ATT CCG TAT
 Asn Met Ala Leu Gly Lys Tyr Val Asp Leu Gly Leu Gly Ile Arg Tyr
 1250 1255 1260
 GAC GTA TCT CGT ACA AAA GCT AAT GAA TCA ACT ATT AGT GTT CGT AAA
 Asp Val Ser Arg Thr Lys Ala Asn Glu Ser Thr Ile Ser Val Gly Lys
 1265 1270 1275
 TTT AAA AAT TTC TCT TCG AAT ACT GGT ATT GTT ATA AAA CCA ACG GAA
 Phe Lys Asn Phe Ser Trp Asn Thr Gly Ile Val Ile Lys Pro Thr Glu
 1280 1285 1290
 TGG CTT GAT CTT TCT TAT CCG CTT TCT ACT GGA TTT AGA AAT CCT AGT
 Thr Leu Asp Leu Ser Tyr Arg Leu Ser Thr Gly Phe Arg Asn Pro Ser
 1295 1300 1305 1310

FIG. 40.

TTT TCT GAA ATG TAT GGT TGG CCG TAT GGT GGC AAG AAT GAC GAG GTT
 Phe Ser Glu Met Tyr Gly Trp Arg Tyr Gly Gly Lys Asn Asp Glu Val
 1315 1320 1325

 TAT GTA GGT AAA TTT AAG CCT GAA ACA TCT CGT AAC CAA GAG TTT GGT
 Tyr Val Gly Lys Phe Lys Pro Glu Thr Ser Arg Asn Gln Glu Phe Gly
 1330 1335 1340

 CTC GCT CTA AAA GGG GAT TTT GGT AAT ATT GAG ATC AGT CAT TTT AGT
 Leu Ala Leu Lys Gly Asp Phe Gly Asn Ile Glu Ile Ser His Phe Ser
 1345 1350 1355

 AAT GCT TAT CGA AAT CTT ATC GCC TTT GCT GAA GAA CTT AGT AAA AAT
 Asn Ala Tyr Arg Asn Leu Ile Ala Phe Ala Glu Glu Leu Ser Lys Asn
 1360 1365 1370

 GGA ACT GGA AAG GGC AAT TAT GGA TAT CAT AAT GCA CAA AAT GCA AAA
 Gly Thr Gly Lys Gly Asn Tyr Gly Tyr His Asn Ala Gln Asn Ala Lys
 1375 1380 1385 1390

 TTA GTT GGC GTA AAT ATA ACT GCA CAA TTA GAT TTT AAT GGT TTA TGG
 Leu Val Gly Val Asn Ile Thr Ala Gln Leu Asp Phe Asn Gly Leu Trp
 1395 1400 1405

FIG. 4P.

AAA CGT ATT CCC TAC GGT TGG TAT GCA ACA TTT GCT TAT AAC CAA GTA
 Lys Arg Ile Pro Tyr Gly Trp Tyr Ala Thr Phe Ala Tyr Asn Gln Val
 1410 1415 1420

AAA GTT AAA GAT CAA AAA ATC AAT GCT TTA GCC TCC GTA AGC AGT
 Lys Val Lys Asp Gln Lys Ile Asn Ala Gly Leu Ala Ser Val Ser Ser
 1425 1430 1435

TAT TTA TTT GAT GCC ATT CAG CCC AGC CGT TAT ATC ATT GGT TTA GGC
 Tyr Leu Phe Asp Ala Ile Gln Pro Ser Arg Tyr Ile Ile Gly Leu Gly
 1440 1445 1450

TAT GAT CAT CCA AGT AAT ACT TGG GGA ATT AAT ACA ATG TTT ACT CAA
 Tyr Asp His Pro Ser Asn Thr Trp Gly Ile Asn Thr Met Phe Thr Gln
 1455 1460 1465 1470

TCA AAA GCA AAA TCT CAA AAT GAA TTG CTA GGA AAA CGT GCA TTA GGT
 Ser Lys Ala Lys Ser Gln Asn Glu Leu Leu Gly Lys Arg Ala Leu Gly
 1475 1480 1485

AAC AAT TCA AGG GAT GTA AAA TCA ACA AGA AAA CTT ACT CGG GCA TGG
 Asn Asn Ser Arg Asp Val Lys Ser Thr Arg Lys Leu Thr Arg Ala Trp
 1490 1495 1500

FIG.4Q.

CAT ATC TTA GAT GTA TCG GGT TAT TAC ATG GCG AAT AAA AAT ATT ATG
His Ile Leu Asp Val Ser Gly Tyr Tyr Met Ala Asn Lys Asn Ile Met
1505 1510 1515

CTT CGA TTA GCG ATA TAT AAT TTA TTC AAC TAT CCG TAT GTT ACT TCG
Leu Arg Leu Gly Ile Tyr Asn Leu Phe Asn Tyr Arg Tyr Val Thr Trp
1520 1525 1530 1535

GAA GCG GTG GGT CAA ACA GCA CAA GGT GCG GTC AAT CAA CAT CAA AAT
Glu Ala Val Arg Gln Thr Ala Gln Gly Ala Val Asn Gln His Gln Asn
1535 1540 1545 1550

GTT GGT AGC TAT ACT CCG TAC GCA GCA TCA GCA AAC TAT ACC TTA
Val Gly Ser Tyr Thr Arg Tyr Ala Ala Ser Gly Arg Asn Tyr Thr Leu
1555 1560 1565

ACA TTA GAA ATG AAA TTC TAAATTA AAA TCGCGCAGAT GCACTAGATA
Thr Leu Glu Met Lys Phe
1570

TGCTATATCT ATACCTTACT GCGCGCATCTT TTCTGTCTCT ATATCTGCT TAAGTGA AAA

ACCAAACTTG CATTITTTAC AAGATCTTTT CACACATTTA TTC

FIG.5A.

ATTTCGTTTGA GCGCATTTTTC CATATTTTAT CCATGAACCTT AAAAAACCTCT AACTTGACAT ⁻³⁵
 TATTTACAAA AAAGATCAAT ⁻¹⁰ AATCGCAATT ATTATCAATT TTGTATGAGT ATATATCTCT ⁻⁶⁰⁵
 ATG AAA TCT GTA CCT CTT ATC TCT GGT GGA CTT TCC TTT TTA CTA AGT
 Met Lys Ser Val Pro Leu Ile Ser Gly Gly Leu Ser Phe Leu Leu Ser 15
 1 5 10
 GCT TGT AGC GGA GGG TCT TTT GAT GTA GAT AAC GTC TCT AAT ACC
 Ala Cys Ser Gly Gly Gly Ser Phe Asp Val Asp Asn Val Ser Asn Thr 30
 20 25
 CCC TCT TCT AAA CCA CGT TAT CAA GAC GAT ACC TCG AAT CAA ACA AAA
 Pro Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr Ser Asn Gln Arg Lys 45
 35 40
 AAA TCT AAT TTG AAA AAG TTG TTC ATT CCT TCT TTA GGA GGA GGG ATG
 Lys Ser Asn Leu Lys Lys Leu Phe Ile Pro Ser Ser Leu Gly Gly Met 60
 50 55
 AAA TTG GUG GCT CAG AAT CTT CGT AAT AAA GAA CCT AGT TTC TTA
 Lys Leu Val Ala Gln Asn Leu Arg Gly Asn Lys Glu Pro Ser Phe Leu 80
 65 70 75 80

FIG. 5B.

AAT GAA GAT GAC TAT ATA TCA TAT TTT TCC TCA CTT TCT ACG ATT GAA
Asn Glu Asp Tyr Ile Ser Tyr Phe Ser Ser Leu Ser Thr Ile Glu
90 95

AAG GAT GTT AAA GAT AAC AAT AAA AAC GCG GCG GAC CTT ATT GCG TCA
Lys Asp Val Lys Asp Asn Asn Lys Asn Gly Ala Asp Leu Ile Gly Ser
100 105 110

ATA GAC GAG CCT AGT ACA ACA AAT CCA CCC GAA AAG CAT CAT GCA CAA
Ile Asp Glu Pro Ser Thr Thr Asn Pro Pro Glu Lys His His Gly Gln
115 120 125

AAA TAT GTA TAT TCA GCG CTT TAT TAT ACT CCA TCG TCG AGT TTA AAC
Lys Tyr Val Tyr Ser Gly Leu Tyr Tyr Thr Pro Ser Thr Ser Leu Asn
130 135 140

GAT TCT AAA AAC AAG TTT TAT TTA GGT TAC TAT GGA TAT GCG TTT TAT
Asp Ser Lys Asn Lys Phe Tyr Leu Gly Tyr Tyr Gly Tyr Ala Phe Tyr
145 150 155 160

TAT GGT AAT AAA ACT GCA ACA AAC TTG CCA GTA AAC GGT GTA GCT AAA
Tyr Gly Asn Lys Thr Ala Thr Asn Leu Pro Val Asn Gly Val Ala Lys
165 170 175

FIG. 5C.

TAC AAA GGA ACT TGG GAT TTC ATC ACT GCA ACT AAA AAT GGC AAA CGT
Tyr Lys Gly Thr Trp Asp Phe Ile Thr Ala Thr Lys Asn Gly Lys Arg
180 185 190

TAT CCT TTG TTA AGT AAT GGC AGT CAC GCT TAT TAT CGA CGT AGT GCA
Tyr Pro Leu Leu Ser Ser Asn Gly Ser His Ala Tyr Tyr Arg Arg Ser Ala
195 200 205

ATT CCA GAA GAT ATT GAT TTA GAA AAT GAT TCA AAG AAT GGT GAT ATA
Ile Pro Glu Asp Ile Asp Leu Glu Asn Asp Ser Lys Asn Gly Asp Ile
210 215 220

GCC TTA ATA AGT GAA TTT AGT GCA GAT TTT GGG ACT AAA AAA CTG ACA
Gly Leu Ile Ser Glu Phe Ser Ala Asp Phe Gly Thr Lys Lys Leu Thr
225 230 235 240

GCA CAA CTG TCT TAC ACC AAA AGA AAA ACT AAT AAT CAA CCA TAT GAA
Gly Gln Leu Ser Tyr Thr Lys Arg Lys Thr Asn Asn Gln Pro Tyr Glu
245 250 255

AAG AAA AAA CTC TAT GAT ATA GAT GCC GAT ATT TAT AGT AAT AGA TTC
Lys Lys Lys Leu Tyr Asp Ile Asp Ala Asp Ile Tyr Ser Asn Arg Phe
260 265 270

FIG. 5D.

AGG GGT ACA GTA AAG CCA ACC GAA AAA GAT TCT GAA GAA CAT CCC TTT
 Arg Gly Thr Val Lys Pro Thr Glu Lys Asp Ser Glu Glu His Pro Phe
 275 280 285
 ACC ACG GAG GGA ACA TTA GAA GGT GGT TTT TAT GGG CCT AAT GCT GAA
 Thr Ser Glu Gly Thr Leu Glu Gly Gly Phe Tyr Gly Pro Asn Ala Glu
 290 295 300
 GAA CTA GGG GGG AAA TTT TTA GCT ACG GAT AAC CGA GTT TTT GGG GTA
 Glu Leu Gly Gly Lys Phe Leu Ala Thr Asp Asn Arg Val Phe Gly Val
 305 310 315 320
 TTT AGT GCC AAA GAA ACG GAA ACA AAA AAG GAA GCG TTA TCC AAG
 Phe Ser Ala Lys Glu Thr Glu Glu Thr Lys Lys Glu Ala Leu Ser Lys
 325 330 335
 GAA ACC TTA ATT GAT GGC AAG CTA ATT ACT TTC TCT ACT AAA AAA ACC
 Glu Thr Leu Ile Asp Gly Lys Leu Ile Thr Phe Ser Thr Lys Lys Thr
 340 345 350
 GAT GCA AAA ACC AAT GCA ACA ACC AGT ACC GCA GCT AAT ACA ACA ACC
 Asp Ala Lys Thr Asn Ala Thr Thr Ser Thr Ala Ala Asn Thr Thr Thr
 355 360 365

FIG. 5E.

GAT ACA ACC GGC AAT ACA ATA ACC GAT GAA AAA AAC TTT AAG ACG GAA
 Asp Thr Thr Ala Asn Thr Ile Thr Asp Glu Lys Asn Phe Lys Thr Glu
 370 375 380

GAT ATA TCA AGT TTT GGT GAA GCT GAT TAT CTG TTA ATT GAC AAA TAT
 Asp Ile Ser Ser Phe Thr Val Ala Asp Tyr Leu Leu Ile Asp Lys Tyr
 385 390 395 400

CCT ATT CCA CTT TTA CCT GAT AAA AAT ACT AAT GAT TTC ATA AGT AGT
 Pro Ile Pro Leu Leu Pro Asp Lys Asn Thr Asn Asp Phe Ile Ser Ser
 405 410 415

AAG CAT CAT ACT GTA GGA AAT AAA CCG TAT AAA GIG GAA GCA TGT TGC
 Lys His His Thr Val Gly Asn Lys Arg Tyr Lys Val Glu Ala Cys Cys
 420 425 430

AGT AAT CTA ACC TAT GIG AAA TTT GGT ATG TAT TAT GAA GAC CCA CTT
 Ser Asn Leu Ser Tyr Val Lys Phe Gly Met Tyr Tyr Glu Asp Pro Leu
 435 440 445

AAA GAA AAA GAA ACA GAA ACA GAA ACA GAA ACA GAA AAA GAC AAA GAA
 Lys Glu Lys Glu Thr Glu Thr Glu Thr Glu Thr Lys Asp Lys Glu
 450 455 460

FIG.5F.

AAA GAA AAA GAA AAA GAC AAA GAC AAA GAA CAA AAA ACG GCG GCA ACG
 Lys Glu Lys Lys Glu Lys Asp Lys Lys Glu Lys Gln Thr Ala Ala Thr
 465 470 475 480
 ACC AAC ACT TAT TAT CAA TTC TTA TTA GGT CAC CGT ACT CCC AAG GAC
 Thr Asn Thr Tyr Tyr Gln Phe Leu Leu Gly His Arg Thr Pro Lys Asp
 485 490 495
 GAC ATA CCT AAA ACA GGA AGT GCA AAA TAT CAT GGT AGT TGG TTT GGT
 Asp Ile Pro Lys Thr Lys Thr Gly Ser Ala Lys Tyr His Gly Ser Trp Phe Gly
 500 505 510
 TAT ATT ACT GAC GGT AAG ACA TCT TAC TCC ACC AGT GGT GAT AAG AAA
 Tyr Ile Thr Asp Gly Lys Thr Ser Tyr Ser Pro Ser Gly Asp Lys Lys
 515 520 525
 CCC GAT AAA AAT GCT GTC GCC GAG TTT AAT GTT GAT TTT GCC GAG AAA
 Arg Asp Lys Asn Ala Val Ala Glu Phe Asn Val Asp Phe Ala Glu Lys
 530 535 540
 AAG CTA ACA GCC GAA TTA AAA CGA CAC GAT ACT GGA AAT CCC GTA TTT
 Lys Leu Thr Gly Glu Leu Lys Arg His Asp Thr Gly Asn Pro Val Phe
 545 550 555 560

FIG. 56.

AGT ATT GAG GCA AAC TTT AAT AGT AGT AAT GCC TTC ACT GGT ACA
 Ser Ile Glu Ala Asn Phe Asn Asn Ser Ser Asn Ala Phe Thr Gly Thr
 565 570 575

GCA ACC GCA ACA AAT TTT GTA ATA GAT GGT AAA AAT AGT CAA AAT AAA
 Ala Thr Ala Thr Asn Phe Val Ile Asp Gly Lys Asn Ser Gln Asn Lys
 580 585 590

AAT ACC CCA AAT AAT ATT ACA ACT AAA GTA AAC GCG CCA TTT TAT GCA
 Asn Thr Pro Ile Asn Ile Thr Thr Lys Val Asn Gly Ala Phe Tyr Gly
 595 600 605

CCT AAG GCT TCT GAA TTA GCG GGT TAT TTC ACT TAT AAC GCA AAT TCT
 Pro Lys Ala Ser Glu Leu Gly Gly Tyr Phe Thr Tyr Asn Gly Asn Ser
 610 615 620

ACA GGT ACA AAT TCT GAA AGT TCC TCA ACC GTA TCT TCA TCA TCC AAT
 Thr Ala Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Ser Ser Ser
 625 630 635 640

TCA AAA AAT GCA AGA GCT GCA GTT GTC TTT GGT GCG AGA CAA CAA GTA
 Ser Lys Asn Ala Arg Ala Ala Val Val Phe Gly Ala Arg Gln Gln Val
 645 650 655

FIG.5H.

GAA ACA ACC AAA	TAATGAATA	CTAAAA	ATG ACT AAA	AAA CCC	TAT TTT	
Glu Thr Thr Lys			Met Thr Lys Lys	Pro Tyr Phe		660
						665
CGC CTA AGT ATT	ATT TGT	CIT TTA	ATT TCA	TGC TAT	GTA AAA	GCA
Arg Leu Ser Ile	Ile Ser Cys	Leu Ile Ser	Cys Tyr Val	Val Lys	Ala	670
						675
GAA ACT CAA	AGT ATA	AAA GAT	ACA AAA	GAA GCT	ATA TCA	TCT GAA GTG
Glu Thr Gln Ser	Ile Lys Asp	Thr Lys	Glu Ala Ile	Ser Ser	Glu Val	680
						685
GAC ACT CAA	AGT ACA	GAA GAT	TCA GAA	TTA GAA	ACT ATC	TCA GTC ACT
Asp Thr Gln Ser	Thr Glu Asp	Ser Glu	Leu Thr	Ile Ser	Val Thr	700
						705
GCA GAA AAA	ATA AGA	GAT CGT	AAA GAT	AAT GAA	GTA ACT	GGA CIT GGC
Ala Glu Lys Ile	Arg Asp	Arg Lys	Asp Asn	Glu Val	Thr Gly	Leu Gly
						720
						725
AAA ATT ATC	AAA ACT	AGT GAA	AGT ATC	AGC CGA	GAA CAA	GTA TTA AAT
Lys Ile Ile Lys	Thr Ser	Glu Ser	Ile Ser	Arg Glu	Gln Val	Leu Asn
						735
						740
						745

FIG. 51.

ATT GGT GAT CTA ACA GGC TAT GAT CCA GGC ATT TCA GTT GTA GAA CAA
 Ile Arg Asp Leu Thr Arg Tyr Asp Pro Gly Ile Ser Val Val Glu Gln
 750 755 760
 GGT GGC GGT GCA AGT TCT GCA TAT TCT ATT GGT GTT ATG GAC AGA AAT
 Gly Arg Gly Ala Ser Ser Gly Tyr Ser Ile Arg Gly Met Asp Arg Asn
 765 770 775
 AGA GTT GCT TTA TTA GTA GAT GGT TTA CCT CAA AGC CAA TCT TAT GTA
 Arg Val Ala Leu Leu Val Asp Gly Leu Pro Gln Thr Gln Ser Tyr Val
 780 785 790 795
 GTG CAA AGC CCT TTA GTT GCT GGT TCA GCA TAT TCT GGC ACT GGT GCA
 Val Gln Ser Pro Leu Val Ala Arg Ser Gly Tyr Ser Gly Thr Gly Ala
 800 805 810
 ATT AAT GAA ATT CAA TAT CAA AAT GTA AAG GCC GTC GAA ATA AGC AAG
 Ile Asn Glu Ile Glu Tyr Glu Asn Val Lys Ala Val Glu Ile Ser Lys
 815 820 825
 GCG GCG AGT TCT TCT GAG TAT GGT AAT GGA CCA CTA GCT GGT TCT GTA
 Gly Gly Ser Ser Ser Glu Tyr Gly Asn Gly Ala Leu Ala Gly Ser Val
 830 835 840

FIG. 5J.

ACA TTT CAA AGC AAA TCA GCA GCC GAT ATC TTA GAA GCA AAA TCA
 Thr Phe Gln Ser Lys Ser Ala Ala Asp Ile Leu Glu Gly Asp Lys Ser
 845 855

TGG GGA ATT CAA ACT AAA AAT OCT TAT TCA AGC AAA AAT AAA GGC TTT
 Trp Gly Ile Gln Thr Lys Asn Ala Tyr Ser Ser Lys Asn Lys Gly Phe
 860 865 870 875

ACC CAT TCT TTA GCT GTA GCA GGA AAA CAA GGT GCA TTT GAA GGG CTA
 Thr His Ser Leu Ala Val Ala Gly Lys Gln Gly Gly Phe Glu Gly Leu
 880 885 890

GCC ATT TAC ACT CAA CGA AAT TCA ATT GAA ACC CAA GTC CAT AAA GAT
 Ala Ile Tyr Thr Gln Arg Asn Ser Ile Glu Thr Gln Val His Lys Asp
 895 900 905

GCA TTA AAA GGC GTA CAA AGT TAT GAT CGA TTA ATC GCC ACA ACA GAT
 Ala Leu Lys Gly Val Gln Ser Tyr Asp Arg Leu Ile Ala Thr Thr Asp
 910 915 920

AAA TCT TCA CGA TAC TTT GTG ATA CAA GGT GAG TGT CCA AAT GGT GAT
 Lys Ser Ser Gly Tyr Phe Val Ile Gln Gly Glu Cys Pro Asn Gly Asp
 925 930 935

FIG.5K.

GAC AAG TGT GCA GCC AAG CCA CCT GCG ACT TTA TCC ACC CAA AGC GAA
 Asp Lys Cys Ala Ala Lys Pro Pro Ala Thr Leu Ser Thr Gln Ser Glu
 940 945 950 955

ACC GTA AGC GTT TCA GAT TAT AGC GCG GCT AAC CGT ATC AAA CCT AAT
 Thr Val Ser Val Ser Asp Tyr Thr Gly Ala Asn Arg Ile Lys Pro Asn
 960 965 970

CCA ATG AAA TAT GAA AGC CAG TCT TGG TTT TTA AGA GGA GGG TAT CAT
 Pro Met Lys Tyr Glu Ser Gln Ser Trp Phe Leu Arg Gly Gly Tyr His
 975 980 985

TTT TCT GAA CAA CAT TAT ATT CGT GGT ATT TTT GAA TTC ACA CAA CAA
 Phe Ser Glu Gln His Tyr Ile Gly Gly Ile Phe Glu Phe Thr Gln Gln
 990 995 1000

AAA TTT GAT ATC CGT GAT ATG ACA TTT CCC GCT TAT TTA AGC CCA ACA
 Lys Phe Asp Ile Arg Asp Met Thr Phe Pro Ala Tyr Leu Ser Pro Thr
 1005 1010 1015

GAA AGA CCG GAT GAT AGT AGT CGT TCT TTT TAT CCA ATG CAA GAT CAT
 Glu Arg Arg Asp Asp Ser Arg Ser Phe Tyr Pro Met Gln Asp His
 1020 1025 1030 1035

FIG. 5L.

GGT GCA TAT CAA CAT ATT GAG GAT GGC ACA GGC GTT AAA TAT GCA AGT
Gly Ala Tyr Gln His Ile Glu Asp Gly Arg Gly Val Lys Tyr Ala Ser
1040 1045 1050

GGG CTT TAT TTC GAT GAA CAC CAT ACA AAA CAG CGT GTA GGT ATT GAA
Gly Leu Tyr Phe Asp Glu His His Arg Lys Gln Arg Val Gly Ile Glu
1055 1060 1065

TAT ATT TAC GAA AAT AAG AAC AAA GCG GGC ATC ATT GAC AAA GCA GIG
Tyr Ile Tyr Glu Asn Lys Asn Lys Ala Gly Ile Ile Asp Lys Ala Val
1070 1075 1080

TTA AGT GCT AAT CAA CAA AAC ATC ATA CTT GAC AGT TAT ATG CCA CAT
Leu Ser Ala Asn Gln Gln Asn Ile Ile Leu Asp Ser Tyr Met Arg His
1085 1090 1095

ACG CAT TGC AGT CTT TAT CCT AAT CCA AGT AAG AAT TGC CGC CCA ACA
Thr His Cys Ser Leu Tyr Pro Asn Pro Ser Lys Asn Cys Arg Pro Thr
1100 1105 1110 1115

CTT GAT AAA CCT TAT TCA TAC TAT CGT TCT GAT ACA AAT GTT TAT AAA
Leu Asp Lys Pro Tyr Ser Tyr Tyr Arg Ser Asp Arg Asn Val Tyr Lys
1120 1125 1130

FIG.5M.

GAA AAA CAT AAT ATG TTG CAA TTG AAT TTA GAG AAA AAA ATT CAA CAA
Glu Lys His Asn Met Leu Gln Leu Asn Leu Glu Lys Lys Ile Gln Gln
1135 1140 1145

AAT TGG CTT ACT CAT CAA ATT GTC TTC AAT CTT GGT TTT GAT GAC TTT
Asn Trp Leu Thr His Gln Ile Val Phe Asn Leu Gly Phe Asp Asp Phe
1150 1155 1160

ACT TCA GCG CTT CAG CAT AAA GAT TAT TTA ACT CCA GGT GTT ATC GGT
Thr Ser Ala Leu Gln His Lys Asp Tyr Leu Thr Arg Arg Val Ile Ala
1165 1170 1175

ACG CCA GAT AGT ATT CCA AGG AAA CCT GGT GAA ACT GGT AAA CCA ACA
Thr Ala Asp Ser Ile Pro Arg Lys Pro Gly Glu Thr Gly Lys Pro Arg
1180 1185 1190 1195

AAT GGT TTG CAA TCA CAA CCT TAC TTA TAC CCA AAA CCA GAG CCA TAT
Asn Gly Leu Gln Ser Gln Pro Tyr Leu Tyr Pro Lys Pro Glu Pro Tyr
1200 1205 1210

TTT CCA GGA CAA GAT CAT TGT AAT TAT CAA GGT ACC TOC TCT AAT TAC
Phe Ala Gly Gln Asp His Cys Asn Tyr Gln Gly Ser Ser Asn Tyr
1215 1220 1225

FIG.50.

GAC GAG GTT TAT GTA GGT AAA TTT AAG OCT GAA ACA TCT OGT AAC CAA
 Asp Glu Val Tyr Val Gly Lys Phe Lys Pro Glu Thr Ser Arg Asn Gln
 1325 1330 1335

GAG TTT GGT CTC GCT CTA AAA GGG GAT TTT GGT AAT ATT GAG ATC AGT
 Glu Phe Gly Leu Ala Leu Lys Gly Asp Phe Gly Asn Ile Glu Ile Ser
 1340 1345 1350 1355

CAT TTT AGT AAT GCT TAT OGA AAT CTT ATC GCC TTT GCT GAA GAA CTT
 His Phe Ser Asn Ala Tyr Arg Asn Leu Ile Ala Phe Ala Glu Glu Leu
 1360 1365 1370

AGT AAA AAT GCA ACT GCA AAG GCC AAT TAT OGA TAT CAT AAT GCA CAA
 Ser Lys Asn Gly Thr Gly Lys Gly Asn Tyr Gly Tyr His Asn Ala Gln
 1375 1380 1385

AAT GCA AAA TTA GTT GGC GTA AAT ATA ACT GCA CAA TTA GAT TTT AAT
 Asn Ala Lys Leu Val Gly Val Asn Ile Thr Ala Gln Leu Asp Phe Asn
 1390 1395 1400

GGT TTA TGG AAA CGT ATT CCC TAC GGT TGG TAT GCA ACA TTT GCT TAT
 Gly Leu Trp Lys Arg Ile Pro Tyr Gly Trp Tyr Ala Thr Phe Ala Tyr
 1405 1410 1415

FIG. 5P.

AAC CAA GTA AAA GTT AAA GAT CAA AAA ATC AAT GCT GGT TTA GCC TCC
Asn Gln Val Lys Val Lys Asp Gln Lys Ile Asn Ala Gly Leu Ala Ser
1420 1425 1430 1435
GTA AGC AGT TAT TTA TTT GAT GCC ATT CAG CCC ACC GGT TAT ATC ATT
Val Ser Ser Tyr Leu Phe Asp Ala Ile Gln Pro Ser Arg Tyr Ile Ile
1440 1445 1450
GGT TTA GGC TAT GAT CAT CCA AGT AAT ACT TGG GGA ATT AAT ACA ATG
Gly Leu Gly Tyr Asp His Pro Ser Asn Thr Trp Gly Ile Asn Thr Met
1455 1460 1465
TTT ACT CAA TCA AAA GCA AAA TCT CAA AAT GAA TTG CTA GGA AAA CGT
Phe Thr Gln Ser Lys Ala Lys Ser Arg Asp Val Lys Leu Gly Lys Arg
1470 1475 1480
GCA TTA GGT AAC AAT TCA AGG GAT GTA AAA TCA ACA AGA AAA CTT ACT
Ala Leu Gly Asn Asn Ser Arg Asp Val Lys Ser Thr Arg Lys Leu Thr
1485 1490 1495
CCG CCA TGG CAT ATC TTA GAT GTA TCG GGT TAT TAC ATG CCG AAT AAA
Arg Ala Trp His Ile Leu Asp Val Ser Gly Tyr Tyr Met Ala Asn Lys
1500 1505 1510 1515

FIG.5Q.

AAT ATT ATG CTT CGA TTA GGG ATA TAT AAT TTA TTC AAC TAT CGC TAT
Asn Ile Met Leu Arg Leu Gly Ile Tyr Asn Leu Phe Asn Tyr Arg Tyr
1525 1530

GTT ACT TGG GAA GCG GTG CGT CAA ACA GCA CAA GGT GCG GTC AAT CAA
Val Thr Trp Glu Ala Val Arg Gln Thr Ala Gln Gly Ala Val Asn Gln
1535 1540 1545

CAT CAA AAT GTT GGT AGC TAT ACT CGC TAC GCA GCA TCA GGA CGA AAC
His Gln Asn Val Gly Ser Tyr Thr Arg Tyr Ala Ala Ser Gly Arg Asn
1550 1555 1560

TAT ACC TTA ACA TTA GAA ATG AAA TTC TAAATTAAAA TGGGCGAGAT
Tyr Thr Leu Thr Leu Glu Met Lys Phe
1565 1570

GGACTAGATA TGCTATATCT ATPACCTACT GGGGCACTT TTTCGTCTCT ATAACTCTCT

TAACTGAAAA ACCAAACTTG GATTCTTAC AAGATCTTTT CACACATTTA TTGTAAATC

TCCGCAATT TTGACCG

FIG. 6 A.

AAAATTCGGT AATGATTAACC CTTATTAATGA TAAGACAGAA AGTTCGTTTAA CCCAATTTTT
 CATATTTTAT CCATGAACCTT AAAAAATTCCT AAGTTCACAT TATTACAAAA AAAGACAAT
 AATCGCAATT ATTATCAATTT TTGTATAGT ATTAAATCT ATG AAA TCT GTA CCT
 Met Lys Ser Val Pro
 1 5
 CTT ATC ACT GGT GGA CTT TCC TTT TTA CTA AGC GCT TGT AGC GGG GGA
 Leu Ile Thr Gly Gly Leu Ser Phe Leu Leu Ser Ala Cys Ser Gly Gly
 10 15 20
 GGT GGT TCT TTT GAT GTA GAT GAC GTC TCT AAT CCC TCC TCT TCT AAA
 Gly Gly Ser Phe Asp Val Asp Asp Val Ser Asn Pro Ser Ser Ser Lys
 25 30 35
 CCA CGT TAT CAA GAC GAT ACC TCG AAT CAA AGA ACA AAA TCT GAT TTG
 Pro Arg Tyr Gln Asp Asp Thr Ser Asn Gln Arg Thr Lys Ser Asp Leu
 40 45 50
 GAA AAG TTG TTC ATT CCT TCT TTA GGG GGA GGG ATG AAG TTA GTG GCT
 Glu Lys Leu Phe Ile Pro Ser Leu Gly Gly Met Lys Leu Val Ala
 55 60 65

FIG.6B.

CAG AAT TTT ATT GGT GCT AGA GAA CCT AGT TTC TTA AAT GAA GAT GGC
Gln Asn Phe Ile Gly Ala Arg Glu Pro Ser Phe Leu Asn Glu Asp Gly 85
70 75 80

TAT ATG ATA TTT TCC TCA CTT TCT ACG ATT GAA GAG GAT GTT GAA AAA
Tyr Met Ile Phe Ser Ser Leu Ser Thr Ile Glu Glu Asp Val Glu Lys 100
90 95

GTT AAA AAT AAC AAT AAA AAC GCG AGG CTT ATT GGC TCA ATT GAG
Val Lys Asn Asn Asn Lys Asn Gly Gly Arg Leu Ile Gly Ser Ile Glu 115
105 110

GAA CCT AAT GCA ACA TCA CAA AAT TCT AAT TCA CAA GAA TAC GTT TAT
Glu Pro Asn Gly Thr Ser Gln Asn Ser Asn Ser Gln Glu Tyr Val Tyr 130
120 125

TCT GGT TTG TAT TAT ATC GAT AGT TGG CGT GAT TAT AAG AAG GAA GAG
Ser Gly Leu Tyr Tyr Ile Asp Ser Trp Arg Asp Tyr Lys Lys Glu Glu 145
135 140

CAG AAA GCT TAT ACT GGC TAT TAT GGT TAT GCA TTT TAT TAT GGT AAT
Gln Lys Ala Tyr Thr Gly Tyr Tyr Gly Tyr Ala Phe Tyr Tyr Gly Asn 165
150 155 160

FIG. 6C.

GAA ACT GCA AAA AAC TTG CCA GTA AAA GGT GTA GCT AAA TAC AAA CGA
 Glu Thr Ala Lys Asn Leu Pro Val Lys Gly Val Ala Lys Tyr Lys Gly
 170 175 180

AGC TGG AAC TTC ATC ACT GCA ACT GAA AAT GGC AAA CGT TAT TCT TTG
 Thr Trp Asn Phe Ile Thr Ala Thr Glu Asn Gly Lys Arg Tyr Ser Leu
 185 190 195

TTC AGT AAT TCT ATC GGT CAA GCT TAT TCC AGA CCG AGC GCT ATT TCA
 Phe Ser Asn Ser Ile Gly Gln Ala Tyr Ser Arg Arg Ser Ala Ile Ser
 200 205 210

GAA GAT ATC TAT AAT TTA GAA AAC GGT GAC GCG GCG TTA ATA AGT GAA
 Glu Asp Ile Tyr Asn Leu Glu Asn Gly Asp Ala Gly Leu Ile Ser Glu
 215 220 225

TTT AGT GTA GAT TTT GGT AAG AAA GAG CTC ACT GCA GAA CTT TAT TAT
 Phe Ser Val Asp Phe Gly Lys Lys Glu Leu Thr Gly Glu Leu Tyr Tyr
 230 235 240 245

AAT GAA AGG AAA ACA AGT GTT AAT GAA TCA CAA AAT ACA ACA CAT AAA
 Asn Glu Arg Lys Thr Ser Val Asn Glu Ser Gln Asn Thr Thr His Lys
 250 255 260

FIG. 6D.

CTC TAC ACT CTA GAA GCT AAA GTG TAT AGC AAC CCA TTC AGA GGT AAA
 Leu Tyr Thr Leu Glu Ala Lys Val Tyr Ser Asn Arg Phe Arg Gly Lys
 265 270 275

GTA AAG CCA ACC AAA ACA AAG TCT GAA GAT CAT CCC TTT ACC AGC GAG
 Val Lys Pro Thr Lys Thr Lys Ser Glu Asp His Pro Phe Thr Ser Glu
 280 285 290

GCA ACA TTA GAA GGT GGT TTT TAT GGG CCT AAT GCT GAA GAA CTA GGG
 Gly Thr Leu Glu Gly Gly Phe Tyr Gly Pro Asn Ala Glu Glu Leu Gly
 295 300 305

GCA AAG TTT TTA GCT AAC GAC GAA AAA GTT TTT GGG GTA TTT AGT GGC
 Gly Lys Phe Leu Ala Asn Asp Glu Lys Val Phe Gly Val Phe Ser Ala
 310 315 320 325

AAA GAA GAC CCA CAA AAC CCA GAA AAC CAA AAA TTA TCC ACA GAA ACC
 Lys Glu Asp Pro Gln Asn Pro Glu Asn Gln Lys Leu Ser Thr Glu Thr
 330 335 340

TTA ATT GAT GGC AAG CTA ATT ACT TTT AAA AGA ACT GAT GCA ACA ACC
 Leu Ile Asp Gly Lys Leu Ile Thr Phe Lys Arg Thr Asp Ala Thr Thr
 345 350 355

FIG.6E.

AAT GCA ACA ACC GAT GCA AAA ACC AGT GCA ACA ACC GAT GCA ACC AGT
 Asn Ala Thr Thr Asp Ala Lys Thr Ser Ala Thr Thr Asp Ala Thr Ser
 360 365 370
 ACA ACA GGC AAT AAA AAA ACC GAT GCA GAA AAC TTT AAG ACG GAA GAT
 Thr Thr Ala Asn Lys Lys Thr Asp Ala Glu Asn Phe Lys Thr Glu Asp
 375 380 385
 ATA CCA AGT TTT GGT GAA GCT GAT TAC CTT TTA ATT GGC AAT CAG CCT
 Ile Pro Ser Phe Gly Glu Ala Asp Tyr Leu Ile Gly Asn Gln Pro
 390 395 400 405
 AIT CCT CTT TTA CCT GAA AAA AAT ACT GAT GAT TTC ATA AGT AGT AAG
 Ile Pro Leu Leu Pro Glu Lys Asn Thr Asp Asp Phe Ile Ser Ser Lys
 410 415 420
 CAC CAT ACG GTA GCA GGT AAA ACC TAT AAA GTA GAA CCA TGT TCC AAG
 His His Thr Val Gly Gly Lys Thr Tyr Lys Val Glu Ala Cys Cys Lys
 425 430 435
 AAT CTA AGC TAT GTG AAA TTT GGT ATG TAT TAT CAG GAT AAA GAT AAG
 Asn Leu Ser Tyr Val Lys Phe Gly Met Tyr Tyr Glu Asp Lys Asp Lys
 440 445 450

FIG.6F.

GAC AAC AAA AAT GAA ACA GAC AAA GAA AAA GGC AAA GAA AAA CCA ACG
 Asp Asn Lys Asn Glu Thr Asp Lys Glu Lys Gly Lys Glu Lys Pro Thr
 455 465

ACG ACA ACA TCCT ATC AAC ACT TAT TAT CAA TTC TTA TTA GGT CTC CGT
 Thr Thr Thr Ser Ile Asn Thr Tyr Tyr Phe Leu Leu Gly Leu Arg
 470 475 480 485

ACT CCC AAG GAC GAA ATA CCT AAA GAA GGA AGT GCA AAA TAT CAT GGT
 Thr Pro Lys Asp Glu Ile Pro Lys Glu Gly Ser Ala Lys Tyr His Gly
 490 495 500

AAT TGG TTT GGT TAT ATT AGT GAT GGC GAG ACA TCT TAC TCC GCC AGT
 Asn Trp Phe Gly Tyr Ile Ser Asp Gly Glu Thr Ser Tyr Ser Ala Ser
 505 510 515

GGT GAT AAG GAA CCC AGT AAA AAT GCT GTC GCC GAG TTT GAT GTA AGT
 Gly Asp Lys Glu Arg Ser Lys Asn Ala Val Ala Glu Phe Asp Val Ser
 520 525 530

TTT GCC AAT AAA ACA TTA ACA GCC GAA TTA AAA CCA CAC GAT AAT GGA
 Phe Ala Asn Lys Thr Leu Thr Gly Glu Leu Lys Arg His Asp Asn Gly
 535 540 545

FIG. 66.

AAT ACC GTA TTT AAA ATT AAT GCA GAA TTA AAT GGT AGT AAT GAC TTC
 Asn Thr Val Phe Lys Ile Asn Ala Glu Leu Asn Gly Ser Asn Asp Phe
 550 555 560 565
 ACT GGT ACA GCA ACC GCA ACA AAT TTT GTA ATA GAT GGT AAC AAT AGT
 Thr Gly Thr Ala Thr Ala Thr Asn Phe Val Ile Asp Gly Asn Asn Ser
 570 575 580
 CAA ACT TCA AAT GCC AAA ATT AAT ATT ACA ACT AAA GTA AAT GCG GCA
 Gln Thr Ser Asn Ala Lys Ile Asn Ile Thr Thr Lys Val Asn Gly Ala
 585 590 595
 TTT TAT GGA CCT AAG CTT TCT GAA TTA GGA GGG TAT TTC ACC TAT AAC
 Phe Tyr Gly Pro Lys Ala Ser Glu Leu Gly Tyr Phe Thr Tyr Asn
 600 605 610
 GGA AAA AAT CCT ACA GCT ACA AAT TCT GAA AGT TCC TCA ACC GTA CCT
 Gly Lys Asn Pro Thr Ala Thr Asn Ser Glu Ser Ser Thr Val Pro
 615 620 625
 TCA CCA CCC AAT TCA CCA AAT GCA AGC GCT GCA GTT GTC TTT GGT GCT
 Ser Pro Pro Asn Ser Pro Asn Ala Ser Ala Ala Val Val Phe Gly Ala
 630 635 640 645

FIG.6H.

AAA AAA GAA GTA GAA ACA ACC AAC TAAAAACAAC CAAGTAATGG

Lys Lys Gln Val Glu Thr Thr Asn Lys

650

AAATCACTAAAA ATG ACT AAA AAA CCC TAT TTT CCC CTA AGT ATT ATT TCT

Met Thr Lys Lys Pro Tyr Phe Arg Leu Ser Ile Ile Ser

655

660

665

TGT CTT TTA ATT TCA TGC TAT GTA AAA GCA GAA ACT CAA AGT ATA AAA

Cys Leu Leu Ile Ser Cys Tyr Val Lys Ala Glu Thr Gln Ser Ile Lys

670

675

680

GAT ACA AAA GAA GCT ATA TCA TCT GAA GTG GAC ACT CAA AGT ACA GAA

Asp Thr Lys Glu Ala Ile Ser Ser Glu Val Asp Thr Gln Ser Thr Glu

685

690

695

GAT TCA GAA TTA GAA ACT ATC TCA GTC ACT GCA GAA AAA ATA AGA GAT

Asp Ser Glu Leu Glu Thr Ile Ser Val Thr Ala Glu Lys Ile Arg Asp

700

705

710

715

CGT AAA GAT AAT GAA GTA ACT CGA CTT CCC AAA ATT ATC AAA ACT AGT

Arg Lys Asp Asn Glu Val Thr Gly Leu Glu Lys Ile Ile Lys Thr Ser

720

725

730

FIG. 6I.

GAA AGT ATC AGC CGA GAA CAA GTA TTA AAT ATT GGT GAT CTA ACA CGC
 Glu Ser Ile Ser Arg Glu Gln Val Leu Asn Ile Arg Asp Leu Thr Arg 735
 740

TAT GAT CCA GGC ATT TCA GTT GTA GAA CAA GGC GGT GGT CCA AGT TCT
 Tyr Asp Pro Gly Ile Ser Val Val Glu Gln Gly Arg Gly Ala Ser Ser 750
 755

GGA TAT TCT ATT GGT GGT ATG GAC AGA AAT AGA GTT GCT TTA TTA GTA
 Gly Tyr Ser Ile Arg Gly Met Asp Arg Asn Arg Val Ala Leu Leu Val 760
 765

GAT GGT TTA CCT CAA AGC CAA TCT TAT GTA GTG CAA AGC CCT TTA GTT
 Asp Gly Leu Pro Gln Thr Gln Ser Tyr Val Val Gln Ser Pro Leu Val 770
 775

GCT GGT TCA GGA TAT TCT GGC ACT GGT GCA ATT AAT GAA ATT GAA TAT
 Ala Arg Ser Gly Tyr Ser Gly Thr Gly Ala Ile Asn Glu Ile Glu Tyr 780
 785

GAA AAT GTA AAG GCC GTC GAA ATA ACC AAG GCG AGT TCT TCT GAG
 Glu Asn Val Lys Ala Val Glu Ile Ser Lys Gly Gly Ser Ser Ser Glu 790
 795

800 805 810 815 820 825

FIG. 6J.

TAT GGT AAT GGA GCA CTA GCT TCT GTT ACA TTT CAA AGC AAA TCA
 Tyr Gly Asn Gly Ala Leu Ala Gly Ser Val Thr Phe Gln Ser Lys Ser
 830 840
 GCA GCC GAT ATC TTA CAA GGA GAC AAA TCA TGG GCA ATT CAA ACT AAA
 Ala Ala Asp Ile Leu Glu Gly Asp Lys Ser Trp Gly Ile Gln Thr Lys
 845 855
 AAT GCT TAT TCA AGC AAA AAT AAA GCC TTT ACC CAT TCT TTA GCT GTA
 Asn Ala Tyr Ser Ser Lys Asn Lys Gly Phe Thr His Ser Leu Ala Val
 860 870 875
 GCT GGA AAA CAA GGG GGA TTT GAC GGG GTC GCC ATT TAT ACT CAA CGA
 Ala Gly Lys Lys Gln Gly Gly Phe Asp Gly Val Ala Ile Tyr Thr Gln Arg
 880 885 890
 AAT TCA ATT GAA ACC CAA GTC CAT AAA GAT GCA TTA AAA GGC GTA CAA
 Asn Ser Ile Glu Thr Gln Val His Lys Asp Ala Leu Lys Gly Val Gln
 895 900 905
 AGT TAT CAT CCA TTA ATC GCC AAA CCA GAG GAT CAA TCT GCA TAC TTT
 Ser Tyr His Arg Leu Ile Ala Lys Pro Glu Asp Gln Ser Ala Tyr Phe
 910 915 920

FIG. 6K.

GTG ATG CAA GAT GAG TGT CCA AAG CCA GAT GAT TAT AAC AGT TGT TTA
 Val Met Gln Asp Glu Cys Pro Lys Pro Asp Tyr Asn Ser Cys Leu
 925 930 935
 CCT TTC GCC AAA CCA CCT GCG ATT TTA TCC TCC CAA AGA GAA ACC GTA
 Pro Phe Ala Lys Arg Pro Ala Ile Leu Ser Ser Gln Arg Glu Thr Val
 940 945 950 955
 AGC GTT TCA GAT TAT ACG GCG GCT AAC CGT ATC AAA CCT AAT CCA ATG
 Ser Val Ser Asp Tyr Thr Gly Ala Asn Arg Ile Lys Pro Asn Pro Met
 960 965 970
 AAA TAT GAA AGC CAG TCT TGG TTT TTA AGA GGA GGG TAT CAT TTT TCT
 Lys Tyr Glu Ser Gln Ser Trip Phe Leu Arg Gly Tyr His Phe Ser
 975 980 985
 GAA CAA CAT TAT ATT GGT GGT ATT TTT GAA TTC ACA CAA CAA AAA TTT
 Glu Gln His Tyr Ile Gly Gly Ile Phe Glu Phe Thr Gln Gln Lys Phe
 990 995 1000
 GAT ATC CGT GAT ATG ACA TTT CCC GCT TAT TTA AGA TCA ACA GAA AAA
 Asp Ile Arg Asp Met Thr Phe Pro Ala Tyr Leu Arg Ser Thr Glu Lys
 1005 1010 1015

FIG. 6L.

CGG GAT GAT AGC AGT GGC TCT TTT TAT CCA AAG CAA GAT TAT GGT CCA
 Arg Asp Asp Ser Ser Gly Ser Phe Tyr Pro Lys Gln Asp Tyr Gly Ala
 1020 1025 1030 1035

TAT CAA CGT ATT GAG GAT GGC CCA GGC GTT AAC TAT CCA AGT GGG CTT
 Tyr Gln Arg Ile Glu Asp Gly Arg Gly Val Asn Tyr Ala Ser Gly Leu
 1040 1045

TAT TTC GAT GAA CAC CAT AGA AAA CAG CGT GTA GGT ATT GAA TAT ATT
 Tyr Phe Asp Glu His His Arg Lys Gln Arg Val Gly Ile Glu Tyr Ile
 1055 1060 1065

TAC GAA AAT AAG AAC AAA GCG GGC ATC ATT GAC AAA CCA GTG TTA AGT
 Tyr Glu Asn Lys Asn Lys Ala Gly Ile Ile Asp Lys Ala Val Leu Ser
 1070 1075 1080

GCT AAT CAA CAA AAC ATC ATA CTT GAC AGT TAT ATG CAA CAT ACG CAT
 Ala Asn Gln Gln Asn Ile Ile Leu Asp Ser Tyr Met Gln His Thr His
 1085 1090 1095

TGC AGT CTT TAT CCT AAT CCA AGT AAG AAT TGC CGC CCA ACA CGT GAT
 Cys Ser Leu Tyr Pro Asn Pro Ser Lys Asn Cys Arg Pro Thr Arg Asp
 1100 1105 1110 1115

FIG. 6M.

AAA CCT TAT TCA TAC TAT CAT TCT GAT AGA AAT GTT TAT AAA GAA AAA
 Lys Pro Tyr Ser Tyr Tyr His Ser Asp Arg Asn Val Tyr Lys Glu Lys
 1120 1125 1130

CAT AAT ATG TTG CAA TTG AAT TTA GAG AAA AAA AAT CAA CAA AAT TGG
 His Asn Met Leu Gln Leu Asn Leu Glu Lys Lys Ile Gln Asn Trp
 1135 1140 1145

CCT ACT CAT CAA AAT GTC TTC AAT CTT GGT TTT GAT GAC TTT ACT TCA
 Leu Thr His Gln Ile Val Phe Asn Leu Gly Phe Asp Asp Phe Thr Ser
 1150 1155 1160

GGG CTT CAG CAT AAA GAT TAT TTA ACT CGA CGT GTT ACC GCT ACG GCA
 Ala Leu Gln His Lys Asp Tyr Leu Thr Arg Arg Val Thr Ala Thr Ala
 1165 1170 1175

AAG AGT ATT TCA GAG AAA GCT AAT CAA ACA AGA AGA AAT GGT TAC AAA
 Lys Ser Ile Ser Glu Lys Ala Asn Glu Thr Arg Arg Asn Gly Tyr Lys
 1180 1185 1190 1195

AAA CAA CCT TAC TTA TAC CCA AAA CCA ACA GTA GGT TTT GTA GTA CAA
 Lys Gln Pro Tyr Leu Tyr Pro Lys Pro Thr Val Gly Phe Val Val Gln
 1200 1205 1210

FIG. 6N.

GAT CAT TGT GAT TAT AAA GGT AAC TCC TCT AAT TAC ACA GAC TGT AAA
 Asp His Cys Asp Tyr Lys Gly Asn Ser Ser Asn Tyr Arg Asp Cys Lys
 1215 1220

GTC CGG TTA ATT AAA GCG AAA AAT TAT TTC GCA GCA CGC AAT AAT
 Val Arg Leu Ile Lys Gly Lys Asn Tyr Tyr Phe Ala Ala Arg Asn Asn
 1230 1235 1240

ATG GCA TTA GCG AAA TAC GTT GAT TTA GGT TTA GGT ATT CCG TAT GAC
 Met Ala Leu Gly Lys Tyr Val Asp Leu Gly Leu Gly Ile Arg Tyr Asp
 1245 1250 1255

GTA TCT CCG ACA AAA GCT AAT GAA TCA ACT ATT AGT GGT AAA TTT
 Val Ser Arg Thr Lys Ala Asn Glu Ser Thr Ile Ser Val Gly Lys Phe
 1260 1265 1270 1275

AAA AAT TTC TCT TGG AAT ACT GGT ATT GTC ATA AAA CCA ACG GAA TGG
 Lys Asn Phe Ser Thr Asn Thr Gly Ile Val Ile Lys Pro Thr Glu Thr
 1280 1285 1290

CTT GAT CTT TCT TAT CCG CTT TCT ACT GCA TTT ACA AAT CCT AGT TTT
 Leu Asp Leu Ser Tyr Arg Leu Ser Thr Gly Phe Arg Asn Pro Ser Phe
 1295 1300 1305

FIG. 60.

GCT GAA ATG TAT GGT TGG CCG TAT GGT GGC AAT AAT AOC GAG GTT TAT
 Ala Glu Met Tyr Gly Trp Arg Tyr Gly Gly Asn Asn Ser Glu Val Tyr
 1310 1315 1320

GTA GGT AAA TTT AAG CCT GAA ACA TCT CGT AAC CAA GAG TTT GGT CTC
 Val Gly Lys Phe Lys Pro Glu Thr Ser Arg Asn Gln Glu Phe Gly Leu
 1325 1330 1335

GCT CTA AAA GGG GAT TTT GGT AAT ATT GAG ATC AGT CAT TTT AGT AAT
 Ala Leu Lys Gly Asp Phe Gly Asn Ile Glu Ile Ser His Phe Ser Asn
 1340 1345 1350 1355

GCT TAT CGA AAT CTT ATC GCC TTT GCT GAA GAA CTT AAT AAA AAT GGA
 Ala Tyr Arg Asn Leu Ile Ala Phe Ala Glu Glu Leu Asn Lys Asn Gly
 1360 1365 1370

ACT GGA AAG GCC AAT TAT GGA TAT CAT AAT GCA CAA AAT GCA AAA TTA
 Thr Gly Lys Ala Asn Tyr Gly Tyr His Asn Ala Gln Asn Ala Lys Leu
 1375 1380 1385

GTT GGC GTA AAT ATA ACT GCG CAA TTA CAT TTT AAT GGT TTA TGG AAA
 Val Gly Val Asn Ile Thr Ala Gln Leu Asp Phe Asn Gly Leu Trp Lys
 1390 1395 1400

FIG. 6P.

CGT ATT CCC TAC GGT TGG TAT GCA ACA TTT GCT TAT AAC CGA GTA AAA
 Arg Ile Pro Tyr Gly Trp Tyr Ala Thr Phe Ala Tyr Asn Arg Val Lys
 1405 1410 1415

GTT AAA GAT CAA AAA ATC AAT GCT GGT TTG GCC TTC GTA AGC AGT TAT
 Val Lys Asp Gln Lys Ile Asn Ala Gly Leu Ala Ser Val Ser Ser Tyr
 1420 1425 1430 1435

TTA TTT GAT GCC ATT CAG CCC AGC CGT TAT ATC ATT GGT TTA GCC TAT
 Leu Phe Asp Ala Ile Gln Pro Ser Arg Tyr Ile Ile Gly Leu Gly Tyr
 1440 1445 1450

GAT CAT CCA AGT AAT ACT TGG GGA ATT AAT ACA ATG TTT ACT CAA TCA
 Asp His Pro Ser Asn Thr Trp Gly Ile Asn Thr Met Phe Thr Gln Ser
 1455 1460 1465

AAA GCA AAA TCT CAA AAT GAA TTG CTA GGA AAA GGT GCA TTG GGT AAC
 Lys Ala Lys Ser Gln Asn Glu Leu Leu Gly Lys Arg Ala Leu Gly Asn
 1470 1475 1480

AAT TCA AGG GAT GTA AAA TCA ACA AGA AAA CTT ACT CGG GCA TGG CAT
 Asn Ser Arg Asp Val Lys Ser Thr Arg Lys Leu Thr Arg Ala Trp His
 1485 1490 1495

FIG. 6Q.

ATC TTA GAT GTA TCG GGT TAT TAC ATG GCG AAT AAA AAT ATT ATG CIT
 Ile Leu Asp Val Ser Gly Tyr Tyr Met Ala Asn Lys Asn Ile Met Leu
 1500 1505 1510 1515

CGA TTA GGG ATA TAT AAT TTA TTC AAC TAT CCG TAT GTT ACT TGG GAA
 Arg Leu Gly Ile Tyr Asn Leu Phe Asn Tyr Arg Tyr Val Thr Trp Glu
 1520 1525 1530

GCG GTG CGT CAA ACA GCA CAA GGT GCG GTC AAT CAA CAT CAA AAT GGT
 Ala Val Arg Gln Thr Ala Gln Gly Ala Val Asn Gln His Gln Asn Val
 1535 1540 1545

GGT AGC TAT ACT CCG TAC GCA TCA GGA CGA AAC TAT ACC TTA ACA
 Gly Ser Tyr Thr Arg Tyr Ala Ala Ser Gly Arg Asn Tyr Thr Leu Thr
 1550 1555 1560

TTA GAA ATG AAA TTCTAAATTA AAATGGCCCA GATGGACTAG ACATGCTATA
 Leu Glu Met Lys
 1565

TCCTATACCTT ACTGGCCAT CTCTTTCTGT TCTATAATCT GGTTAAGTCA AAAACCAAC

TTGGATTTT TAGAAGATCT TTCCAGCCAT TTATTGTAAA ATCTCGACA ATTCTTACCG

CACCTTTC TCATTACAAA ACAATPAGGA TCTCTTTGTG AATCTCTCA

FIG.7 A.

CAACATCTCC CCAAGCTATA TTGGTTAATG ATAGCCTAT TAATGATAAG CCTATTATATG
 ATAGAAGAAG AATTGTGTTTT ACCCCATTTT TCATATTTTA TCCATCAACT TAAAAAATTC
 TTAAGTTGACA TTATTACAAA AAAAGACAA TAATCGCAAT TATTATCAAT TTTGTATTAAG
 AATATTAATTC T ATG AAA TCT GTA CCT CTT ATC TCT GGT GGA CTT TCC TTT
 Met Lys Ser Val Pro Leu Ile Ser Gly Gly Leu Ser Phe
 1 5 10
 TTA TTA AGT GCT TGT ACG GGA GGA GGG TCT TTT GAT GTA GAT AAC GTC
 Leu Leu Ser Ala Cys Ser Gly Gly Gly Ser Phe Asp Val Asp Asn Val
 15 20 25
 TCT AAT CCC TCC TCT TCT AAA CCA CGT TAT CAA GAC GAT ACC TCG AAT
 Ser Asn Pro Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr Ser Asn
 30 35 40 45
 CAA ACA ACA AAA TCT GAT TTG CAA AAG TTG TCC ATT CCT TCT TTA GGG
 Gln Arg Thr Lys Ser Asp Leu Gln Lys Leu Ser Ile Pro Ser Leu Gly
 50 55 60

FIG. 7B.

GCA GCG ATG AAG TTA GTG GCT CAG AAT CTT CTT GGT AAG AAA GAA CCT
 Gly Gly Met Lys Leu Val Ala Gln Asn Leu Leu Gly Lys Lys Glu Pro
 65 70 75

AGT CTC TTA AAT AAT GAA GAT GGC TAT ATG ATA TTT TCC TCA CTT TCT
 Ser Leu Leu Asn Asn Glu Asp Gly Tyr Met Ile Phe Ser Ser Leu Ser
 80 85 90

ACG ATT GAA GAG GAT GTT ACA AAA GAA AAT AAA TCT CAG GAA CCC ACT
 Thr Ile Glu Glu Asp Val Thr Lys Glu Asn Lys Ser Gln Glu Pro Thr
 95 100 105

ATT GGC TCA ATA GAC GAG CCT AGC AAA ACA AAT TCA CCC CAA AAT CAT
 Ile Gly Ser Ile Asp Glu Pro Ser Lys Thr Asn Ser Pro Gln Asn His
 110 115 120 125

CAT GGC AAT ATG TAT ATT CCG GTC TTT ATT ATA TTC AAT CGT GGC GTA
 His Gly Asn Met Tyr Ile Arg Val Phe Ile Ile Phe Asn Arg Gly Val
 130 135 140

ATT CCT CAA ATG GCA AGT TTT ATT CAG GTT ACT ATG GAT ATG CGT ATT
 Ile Pro Gln Met Ala Ser Phe Ile Gln Val Thr Met Asp Met Arg Ile
 145 150 155

FIG.7 C.

ACT TTG GCA AGC AAA CAG CCA CTA CAT TAC CTG TAGATGGCGA AGCAAGGATAT
 Thr Leu Ala Ser Lys Gln Pro Leu His Tyr Leu
 160 165

AAAGGAACATT GGCAGTTCAT CACGGCAACT GAAATGGCA AAAAGTATTC TTGTGTCAGT
 AATCATAGCG GTCAAGCCTA TCCGAGAGCT AGTCCANITC CAGACATATAT TCAATTAGAA
 AAAAAATGATT CAACTAATGG TGCAAGGGC TTAAATAAGTG AATTTAGTGT CAATTTTGGT
 ACAAAAAAC TCACTCGAAA ACTTTATTAT AATGAAGAG AAACAGAACT TAATAATCA
 AAAGATAGAA AACATACACT CTACANITCA GAAGCTGAAG TGTATAGTAA CCGATTCAGG
 GGTACAGTAA AGCCAAOCGA AAAAGATICT ACAGATCATC OCTTTACCAG CGAGGGAACA
 TTACAGAGTG GTTTTATAGG GCGTAAAGGT GAAGAACTAG GAGGAAAGTT TTTAGCTGGC
 GATAAAAAG TTTTGTGGGT ATTATGTGCC AAAGAAACCG AGCAAAACAA AAAGAAACCG
 TTATCCACGG AAACCTTAAT TGATGGCAAG CTAACTACTT TTTAAACAAC CAATGCCACA
 ACCAATGCCA CAGCCATCC AACCAACAGT ACAACGCCA GTACACACAAC CGATCCAGAA

FIG.7 D.

AACTTTACGA CGAAGATAT ACCAAGTTTT GGTCAAGCTG ATTACCTTTT AATTGATAAT
 TACCCIGTTC CTCTTTTACC TCGAGGIGGT GATTTCATAA GTAGTAAGCA CCATACGTGA
 GGAAGAAAA CCTATCAAGT AGAGCATGT TCGAGTAATC TAAGCTATGT GAAATTTGGT
 ATCTTTTATG AAGACCACT TAAAGAGAA AAGACAAG AAAAAGAGA AGACAAGAA
 AAACAAACG CGCAACGAC CAACCTTAT TATCAATCT TATTAGGCT CCGTACTGCC
 AGTTCIGAAA TTCTTAAAT GCGAAGGTC GAATATCGG GTATTGGTT TGGTTATATT
 AGTGTGGA CGACATCTTA CTCCCCAGT GGTGATAAG AAGCAATAA AATGCTCC
 GCGATTTTA ATGTTGATTT TGTCAATPAA AAGCTAACG GCACATPAA ACGACAGAT
 AATGGAATA CCGTATTTAG TATTGAGGA AACTTTAACA GTGGGAATGA CTTCCTGGT
 AAAGCAACG CAAAAGATTT AGTATPAGT GTTAAAGTA CACAAGCCAC ATCTAAAGTC
 AATTTCAGG CAACAGTAAA AGGGGCAATTT TATGGAOCTG ATGCTTCTGA ATTAGGGGT
 TATTTCACCT ATAAGCGAAA AATCTTACA GCTACAAATT CCCCACCGT ATCTTCACCA

FIG. 7E.

TCCAATTCAG CAAATGCTGG TCTTCGGTIT GIGTTTGAG CTAAAAACA AGTAGACACA

ACCAACAGT AGAAAAACC AAATTAATGCA ATACTAAA ATG ACT AAA AAA CCC
Met Thr Lys Lys Pro
170

TTAT TTT GCG CTA AGT ATT ATT TCT TGT CTT TTA ATT TCA TGC TAT GTA
Tyr Phe Arg Leu Ser Ile Ile Ser Cys Leu Leu Ile Ser Cys Tyr Val
175 180 185

AAA GCA GAA ACT CAA AGT ATA AAA GAT ACA AAA GAA GCT ATA TCA TCT
Lys Ala Glu Thr Gln Ser Ile Lys Asp Thr Lys Glu Ala Ile Ser Ser
190 195 200 205

GAA GTG GAC ACT CAA AGT ACA GAA GAT TCA GAA TTA GAA ACT ATC TCA
Glu Val Asp Thr Gln Ser Thr Glu Asp Ser Glu Leu Glu Thr Ile Ser
210 215 220

GTC ACT GCA GAA AAA ATA AGA GAT CGT AAA GAT AAT GAA GTA ACT GGA
Val Thr Ala Glu Lys Ile Arg Asp Arg Lys Asp Asn Glu Val Thr Gly
225 230 235

CTT GGC AAA ATT ATA AAA ACG AGT GAA AGT ATC AGC CGA GAA CAA GTA
Leu Gly Lys Ile Ile Lys Thr Ser Glu Ser Ile Ser Arg Glu Gln Val
240 245 250

FIG.7F.

TTA AAT ATT CGT GAT CTA ACA GGC TAT GAT CCA GGC ATT TCA GTT GTA
 Leu Asn Ile Arg Asp Leu Thr Arg Tyr Asp Pro Gly Ile Ser Val Val
 255 260 265
 GAA CAA GGT CGC GGT GCA AGT TCT GGA TAT TCT ATT CGT GGT ATG GAC
 Glu Gln Gly Arg Gly Ala Ser Ser Gly Tyr Ser Ile Arg Gly Met Asp
 270 275 280 285
 AGA AAT AGA GTT GCT TTA TTA GTA GAT GGT TTA CCT CAA ACG CAA TCT
 Arg Asn Arg Val Ala Leu Leu Val Asp Gly Leu Pro Gln Thr Gln Ser
 290 295 300
 TAT GTA GTG CAA ACG CCT TTA GTT GCT CGT TCA GGA TAT TCT GGC ACT
 Tyr Val Val Gln Ser Pro Leu Val Ala Arg Ser Gly Tyr Ser Gly Thr
 305 310 315
 GGT GCA ATT AAT GAA ATT GAA TAT GAA AAT GTA AAG GCC GTC GAA ATA
 Gly Ala Ile Asn Glu Ile Glu Tyr Glu Asn Val Lys Ala Val Glu Ile
 320 325 330
 ACG AAG GGG GGG AGT TCT TCT GAG TAT GGT AAT GGA CTA CTA GCT GGT
 Ser Lys Gly Gly Ser Ser Ser Glu Tyr Gly Asn Gly Ala Leu Ala Gly
 335 340 345

FIG. 76.

TCT GTA ACA TTT CAA AGC AAA TCC GCA GGC GAT ATC TTA GAA GGA GAC
 Ser Val Thr Phe Gln Ser Lys Ser Ala Ala Asp Ile Leu Glu Gly Asp 365
 350
 AAA TCA TGG GGA ATT CAA ACT AAA AAT GCT TAT TCA AGC AAA AAT AAA
 Lys Ser Trp Gly Ile Gln Thr Lys Asn Ala Tyr Ser Ser Lys Asn Lys 380
 370
 GGC TTT ACC CAT TCT TTA GCT GTA GCA AAA CAA GGT GGA TTT GAA
 Gly Phe Thr His Ser Leu Ala Val Ala Gly Lys Gln Gly Gly Phe Glu 395
 385
 GGG GTC GCC ATT TAC ACT CAA CGA AAT TCG GAG GAA ACC CAA GTC CAT
 Gly Val Ala Ile Tyr Thr Gln Arg Asn Ser Glu Glu Thr Gln Val His 410
 400
 AAA GAT GCA TTA AAA GGC GTA CAA AGT TAT GAG CGA TTC ATC GCC ACA
 Lys Asp Ala Leu Lys Gly Val Gln Ser Tyr Glu Arg Phe Ile Ala Thr 425
 415
 ACA GAT AAA TCT TCA GGA TAC TTT GTG ATA CAA GGT GAG TGT CCA AAT
 Thr Asp Lys Ser Ser Gly Tyr Phe Val Ile Gln Gly Glu Cys Pro Asn 445
 430

FIG. 7H.

GGT GAT GAC AAG TGT GCA GCC AAA CCA CCT GCA AAG TTA TCC CCC CAA
 Gly Asp Asp Lys Cys Ala Ala Lys Pro Pro Ala Lys Leu Ser Pro Gln
 455 460

AGC GAA ACC GTA ACC GTT TCA GAT TAT ACG GCG GCT AAC CGT ATC AAA
 Ser Glu Thr Val Ser Val Ser Asp Tyr Thr Gly Ala Asn Arg Ile Lys
 465 470 475

CCT AAT CCA ATG AAA TAT GAA ACC CAG TCT TCG TTT TTA AGA GGA GGG
 Pro Asn Pro Met Lys Tyr Glu Ser Gln Ser Trp Phe Leu Arg Gly Gly
 480 485 490

TAT CAT TTT TCT GAA CAA CAC TAT ATT GGT GGT ATT TTT GAA TTC ACA
 Tyr His Phe Ser Glu Gln His Tyr Ile Gly Gly Ile Phe Glu Phe Thr
 495 500 505

CAA CAA AAA TTT GAT ATC CGT GAT ATG ACA TTT CCC GCT TAT TTA AGA
 Gln Gln Lys Phe Asp Ile Arg Asp Met Thr Phe Pro Ala Tyr Leu Arg
 510 515 520 525

TCA ACA GAA AAA CCG GAT GAT AGA ACT CCC CCT TTT TAT CCA AAG CAA
 Ser Thr Glu Lys Arg Asp Asp Arg Thr Gly Pro Phe Tyr Pro Lys Gln
 530 535 540

FIG.71.

GAT TAT GGT GCA TAT CAA CGT ATT GAG CAT GGC CGA GGC GTT AAC TAT
 Asp Tyr Gly Ala Tyr Gln Arg Ile Glu Asp Gly Val Asn Tyr
 545 550 555

GCA AGT GGG CTT TAT TTC GAT GAA CAC CAT ACA AAA CAG CGT GTA GGT
 Ala Ser Gly Leu Tyr Phe Asp Glu His Arg Lys Gln Arg Val Gly
 560 565 570

ATT GAA TAT ATT TAC GAA AAT AAG AAC AAA GCG GGC ATC ATT GAC AAA
 Ile Glu Tyr Ile Tyr Glu Asn Lys Asn Lys Ala Gly Ile Ile Asp Lys
 575 580 585

GCA GTG TTA AGT GCT AAT CAA CAA AAC ATC ATA CTT GAC AGT TAT ATG
 Ala Val Leu Ser Ala Asn Gln Gln Asn Ile Ile Leu Asp Ser Tyr Met
 590 595 600 605

GCA CAT ACG CAT TGC AGT CTT TAT CCT AAT CCA AGT AAG AAT TGC CGC
 Arg His Thr His Cys Ser Leu Tyr Pro Asn Pro Ser Lys Asn Cys Arg
 610 615 620

CCG ACA CTT GAT AAA CCT TAT TCA TAC TAT CGT TCT GAT ACA AAT GTT
 Pro Thr Leu Asp Lys Pro Tyr Ser Tyr Arg Ser Asp Arg Asn Val
 625 630 635

FIG. 7J.

TAT AAA GAA AAA CAT AAT ATG TTG CAA TTG AAT TTA GAG AAA AAA ATT
Tyr Lys Glu Lys His Asp Met Leu Gln Leu Asn Leu Glu Lys Lys Ile

CAA CAA AAT TGG CTT ACT CAT CAA ATT GTC TTC AAT CTT TTT GAT
Gln Gln Asn Trp Leu Thr His Gln Ile Val Phe Asn Leu Gly Phe Asp
655 660 665

GAC TTT ACT TCA GCG CTT CAG CAT AAA GAT TAT TTA ACT CGA CGT GTT
Asp Phe Thr Ser Ala Leu Gln His Lys Asp Tyr Leu Thr Arg Arg Val
670 675 680 685

ACC GCT ACG GCA AAT ATT ATT TCA GGG ACA GTT GCT GGT AAA CGA AGA
Thr Ala Thr Ala Asn Ile Ile Ser Gly Thr Val Ala Gly Lys Arg Arg 700

Asn Gly Tyr Glu Lys Gln Pro Tyr Leu Tyr Ser Lys Pro Lys Val Asp
705 710 715

TTT GTA GGA CAA GAT CAT TGT AAT TAT AAA GGT AGC TCC TCT AAT TAC
Phe Val Gly Gln Asp His Cys Asn Tyr Lys Gly Ser Ser Ser Asn Tyr

FIG.7K.

ACC GAC TGT AAA GIG CCG TTA ATT AAA GCG AAA AAT TAT TAT TTC CCA
Ser Asp Cys Lys Val Arg Leu Ile Lys Gly Lys Asn Tyr Tyr Phe Ala
735 745

GCA CCG AAT AAT ATG CCA TTA CCG AAA TAC ATT GAT TTA GGT TTA GGT
Ala Arg Asn Asn Met Ala Leu Gly Lys Tyr Ile Asp Leu Gly Leu Gly
750 755 760 765

ATT CCG TAT GAC GTA TCT CGT ACA AAA GCT AAT GAA TCA ACT ATT AGT
Ile Arg Tyr Asp Val Ser Arg Thr Lys Ala Asn Glu Ser Thr Ile Ser
770 775 780

GTT GGT AAA TTT AAA AAT TTC TCT TCG AAT ACT GGT ATT GTC ATA AAA
Val Gly Lys Phe Lys Asn Phe Ser Trp Asn Thr Gly Ile Val Ile Lys
785 790 795

CCA ACG GAA TGG CTT GAT CTT TCT TAT CCG CTT TCT ACT GCA TTT AGA
Pro Thr Glu Trp Leu Asp Leu Ser Tyr Arg Leu Ser Thr Gly Phe Arg
800 805 810

AAT CCT AGT TTT GCT GAA ATG TAT GGT TGG CCG TAT GGT GGC AAT AAT
Asn Pro Ser Phe Ala Glu Met Tyr Gly Trp Arg Tyr Gly Gly Asn Asn
815 820 825

FIG. 7L.

ACC GAT GTT TAT GTA GGT AAA TTT AAG CCT GAA ACA TCT CGT AAC CAA
Ser Asp Val Tyr Val Gly Lys Phe Lys Pro Glu Thr Ser Arg Asn Gln 845
830

GAG TTT GGT CTC GCT CTA AAA GCG GAT TTT GGT AAT ATT GAG ATC AGT
Glu Phe Gly Leu Ala Leu Lys Gly Asp Phe Gly Asn Ile Glu Ile Ser 860
850 855

CAT TTT AGT AAT GCT TAT CGA AAT CTT ATC GCC TTT GCT GAA GAA CTT
His Phe Ser Ser Asn Ala Tyr Arg Asn Leu Ile Ala Phe Ala Glu Glu Leu 875
865 870

AGT AAA AAT CGA ACT ACT CGA AAG GCG AAT TAT CGA TAT CAT AAT GCA
Ser Lys Asn Gly Thr Thr Gly Lys Gly Asn Tyr Gly Tyr His Asn Ala 890
880 885

CAA AAT GCA AAA TTA GTT GCG GTA AAT ATA ACT GCG CAA TTA GAT TTT
Gln Asn Ala Lys Leu Val Gly Val Asn Ile Thr Ala Gln Leu Asp Phe 905
895 900

AAT GGT TTA TGG AAA CGT ATT CCC TAC GGT TGG TAT GCA ACA TTT GCT
Asn Gly Leu Trp Lys Arg Ile Pro Tyr Gly Trp Tyr Ala Thr Phe Ala 925
910 915 920

FIG. 7 M.

TAT AAC CGA GTA AAA GTT AAA GAT CAA AAA ATC AAT GGT GGT TTG GCC
 Tyr Asn Arg Val Lys Val Lys Asp Gln Lys Ile Asn Ala Gly Leu Ala 940
 935
 TTC GTA AGC AGT TAT TTA TTT GAT GCC ATT CAG CCC AGC GGT TAT ATC
 Ser Val Ser Ser Tyr Leu Phe Asp Ala Ile Gln Pro Ser Arg Tyr Ile 955
 950
 ATT GGT TTA GGC TAT GAT CAT CCA AGT AAT ACT TGG CGA ATT AAT ACA
 Ile Gly Leu Gly Tyr Asp His Pro Ser Asn Thr Trp Gly Ile Asn Thr 970
 960
 ATG TTT ACT CAA TCA AAA GCA AAA TCT CAA AAT GAA TTG CTA GCA CAA
 Met Phe Thr Gln Ser Lys Ala Lys Ser Gln Asn Glu Leu Leu Gly Gln 985
 975
 CGT GCA TTG GGT AAC AAT TCA AGG AAT GTA AAA TCA ACA AGA AAA CTT
 Arg Ala Leu Gly Asn Asn Ser Arg Asn Val Lys Ser Thr Arg Lys Leu 1005
 990
 ACT CGG CCA TGG CAT ATC TTA GAT GTA TCG GGT TAT TAC ATG GCG AAT
 Thr Arg Ala Trp His Ile Leu Asp Val Ser Gly Tyr Tyr Met Ala Asn 1020
 1010
 1015

FIG.7 N.

AAA AAT AAT ATG CTT CGA TTA GGG ATA TAT AAT TTA TTC AAC TAT CGC
Lys Asn Ile Met Leu Arg Leu Gly Ile Tyr Asn Leu Phe Asn Tyr Arg
1025 1030 1035

TAT GTT ACT TCG GAA GCG GTG CGT CAA ACA GCA CAA GGT CCG GTC AAT
Tyr Val Thr Trp Glu Ala Val Arg Gln Thr Ala Gln Gly Ala Val Asn
1040 1045 1050

CAA CAT CAA AAT GTT GGT AGC TAT ACT CCG TAC GCA GCA TCA CCA CGA
Gln His Gln Asn Val Gly Ser Tyr Thr Arg Tyr Ala Ala Ser Gly Arg
1055 1060 1065

AAC TAT ACC TTA ACA TTA GAA ATG AAA TTC TAAATTAAAA TCGCCAGAT
Asn Tyr Thr Leu Thr Leu Glu Met Lys Phe
1070 1075

GGACTAGATA TGCATATATCT ATACCTTACT GCGCATCTT TTTCIGTCT ATATCTGCT

TAAATGAAAA ACCAAACTIG GATTTTWTAC AAGATCTTTT CACGCCATTTA TTGTAATAATC

TCCGACAAAT TTTCACCGCAC TTTCCTCTAT TACAAAAACA ATPAGGATCC TTITIGTACT

CTCTCATCT TTGGCAAGTT GCIGTTACAA CTTCAGATCA AGTTTCAGCC ACCGATCTTA

GGCACITGGG TTTCGCC

FIG. 8A:

[illegible]

F16.8B.

AAA GCT GAT GTT GAA AAA GAA AAT AAA CAC TAT ACA AGT CCA GTT GGC
 Lys Ala Asp Val Glu Lys Glu Asn Lys His Tyr Thr Ser Pro Val Gly
 100 105 110

TCA ATA GAC GAG CCT AGT ACA ACA AAT CCA AAA GAA AAT GAT CAT GGA
 Ser Ile Asp Glu Pro Ser Thr Thr Asn Pro Lys Glu Asn Asp His Gly
 115 120 125

CAA AGA TAT GTA TAT TCA GGA CTT TAT TAT ATT CCA TCG TGG AAT TTA
 Gln Arg Tyr Val Tyr Ser Gly Leu Tyr Tyr Ile Pro Ser Trp Asn Leu
 130 135 140

AAC GAT CTT AAA AAT AAC AAG TAT TAT TAT TCT GGT TAC TAT GGA TAT
 Asn Asp Leu Lys Asn Asn Lys Tyr Tyr Ser Gly Tyr Tyr Gly Tyr
 145 150 155

GGC TAT TAC TTT GGC AAG CAA ACA GGC ACT ACA TTA CCT GTA AAT GGC
 Ala Tyr Tyr Phe Gly Lys Gln Thr Ala Thr Thr Leu Pro Val Asn Gly
 160 165 170 175

AAA GTA ACG TAT AAA GGA ACT TGG ACG TTC ATC ACC GCA CCT GAA AAT
 Lys Val Thr Tyr Lys Gly Thr Trp Ser Phe Ile Thr Ala Ala Glu Asn
 180 185 190

FIG.8C.

GCC AAA AGG TAT CCT TTG TTA AGT AAT GGC AGT CAA GCT TAT TTT CGA
Gly Lys Arg Tyr Pro Leu Ser Asn Gly Ser Gln Ala Tyr Phe Arg
195 200 205

CGT AGT GCA ATT CCA GAA GAT ATT GAT TTA GAA GTT AAA AAT GAT GAG
Arg Ser Ala Ile Pro Glu Asp Ile Asp Leu Glu Val Lys Asn Asp Glu
210 215 220

AAT AGA GAA AAA GGG CTA GTG AGT GAA TTT AGT CCA GAT TTT GGG ACT
Asn Arg Glu Lys Gly Leu Val Ser Glu Phe Ser Ala Asp Phe Gly Thr
225 230 235

AAA AAA CTG ACA GGA GGA CTG TTT TAC ACC AAA AGA CAA ACT CAT ATT
Lys Lys Leu Thr Gly Gly Leu Phe Tyr Thr Lys Arg Gln Thr His Ile
240 245 250 255

CAA AAC CAT GAA AAG AAA AAA CTC TAT GAT ATA GAT GCC CAT ATT TAT
Gln Asn His Glu Lys Lys Lys Leu Tyr Asp Ile Asp Ala His Ile Tyr
260 265 270

AGT AAT AGA TTC AGA GGT AAA GTA AAT CCT ACC CAA AAA GAT TCT AAA
Ser Asn Arg Phe Arg Gly Lys Val Asn Pro Thr Gln Lys Asp Ser Lys
275 280 285

FIG. 8D.

GAA CAT CCC TTT ACC ACC GAG GGA ACA TTA GAA GGT GGT TTT TAC GGG
 Glu His Pro Phe Thr Ser Glu Gly Thr Leu Glu Gly Phe Tyr Gly 290 295 300

CCG GAA GGT CAA GAA TTA GGA GGA AAG TTT TTA GCT GGC GAC AAA AAA
 Pro Glu Gly Gln Glu Leu Gly Gly Lys Phe Leu Ala Gly Asp Lys Lys 305 310 315

GTT TTT GGG GTA TTT AGT GCC AAA GGA ACG GAA GAA AAC AAA AAA TTA
 Val Phe Gly Val Phe Ser Ala Lys Gly Thr Glu Glu Asn Lys Lys Leu 320 325 330 335

CCC AAA GAA ACC TTA ATT GAT GGC AAG CTA ACT ACT TTC TCT ACT AAA
 Pro Lys Glu Thr Leu Ile Asp Gly Lys Leu Thr Thr Phe Ser Thr Lys 340 345 350

ACA ACC GAT GCA AAA ACC AAT GCA ACA GCC AAT GCA ACA ACC AGT ACC
 Thr Thr Asp Ala Lys Thr Asn Ala Thr Ala Asn Ala Thr Thr Ser Thr 355 360 365

GCA GCC AAT ACA ACA ACC GAT ACA ACA GCC AAT ACA ATA ACC GAT GCA
 Ala Ala Asn Thr Thr Thr Asp Thr Thr Ala Asn Thr Ile Thr Asp Ala 370 375 380

FIG.8E.

GAA AAC TTT AAG ACG AAA GAT ATA TCA AGT TTT GGT GAA GGT GAT TAC
Glu Asn Phe Lys Thr Lys Asp Ile Ser Phe Gly Glu Ala Asp Tyr
385 395

CTT TTA ATT GAT AAT TAC CCT GGT CCT CTT TTA CCT GAG AGT GGT GAT
Leu Ile Asp Asn Tyr Pro Val Pro Leu Leu Pro Glu Ser Gly Asp
400 410 415

TTC ATA AGT AGT AAG CAC CAT ACT GTA GGA AAG AAA ACC TAT CAA GTA
Phe Ile Ser Ser Lys His His Thr Val Gly Lys Lys Thr Tyr Gln Val
420 425 430

AAA GCA TGT TGC AGT AAT CTA AGC TAT GTG AAA TTT GGT ATG TAT TAT
Lys Ala Cys Cys Ser Asn Leu Ser Tyr Val Lys Phe Gly Met Tyr Tyr
435 440 445

GAA GTC CCA CCT AAA GAA GAA CAC AAA GAA AAA GAA AAA GAA AAA
Glu Val Pro Pro Lys Glu Glu Lys Asp Lys Glu Lys Lys Glu Lys
450 455 460

GAA AAA GAA AAA CAA GCG ACA AAT CTA TCG AAC ACT TAT TAT CAA TTC
Glu Lys Glu Lys Gln Ala Thr Asn Leu Ser Asn Thr Tyr Tyr Gln Phe
465 470 475

FIG.8F.

TTA TTA GGT CTC GGT ACT OCC AGT TCT GAA ATT CCT AAA GGA GGA AGT
 Leu Leu Gly Leu Arg Thr Pro Ser Glu Ile Pro Lys Gly Gly Ser
 480 495
 GCA AAA TAT CTC GGT AGT TGG TTT GGT TAT CTG AGC GAT GGT TCA ACA
 Ala Lys Tyr Leu Gly Ser Trp Phe Gly Tyr Leu Ser Asp Gly Ser Thr
 500 510
 TCT TAC TCC CCC AGT GGT GAT AAG AAA CCC GAG AAC AAT GGT CTC GCC
 Ser Tyr Ser Pro Ser Gly Asp Lys Lys Arg Glu Asn Asn Ala Leu Ala
 515 520 525
 GAG TTT AAT GTA AAT TTT GTC GAT AAA ACA TTA AAA GCC CAA TTA ATA
 Glu Phe Asn Val Asn Phe Val Asp Lys Thr Leu Lys Gly Gln Leu Ile
 530 540 545
 CGA CAC GAT AAT CAA AAT ACC GTT TTT ACA ATT GAT GCA ACC TTT AAA
 Arg His Asp Asn Gln Asn Thr Val Phe Thr Ile Asp Ala Thr Phe Lys
 550 555
 GGT GGT AAG AAT AAC TTC ACT GGT ACA GCA ACC GCA AAC AAT GTA GCG
 Gly Gly Lys Asn Asn Phe Thr Gly Thr Ala Thr Ala Asn Asn Val Ala
 560 570 575

FIG. 8G.

ATT GAT CCC CAA AGT ACA CAA GGC ACA TCT AAC GTC AAT TTC ACG GCA
 Ile Asp Pro Gln Ser Thr Gln Gly Thr Ser Asn Val Asn Phe Thr Ala
 585 590

ACA GTA AAT GGG GCA TTT TAT GGG CCG AAC GCT ACA GAA TTA GGC GGT
 Thr Val Asn Gly Ala Phe Tyr Gly Pro Asn Ala Thr Glu Leu Gly Gly
 595 600 605

TAT TTC ACC TAT AAC GGA AAT CCT ACA GAT AAA AGT TCC TCA ACC GTA
 Tyr Phe Thr Tyr Asn Gly Asn Pro Thr Asp Lys Ser Ser Thr Val
 610 615 620

CCT TCA TCA TCC AAT TCA AAA AAT GCA AGA GCT GCA GTT GTC TTT GGT
 Pro Ser Ser Ser Asn Ser Lys Asn Ala Arg Ala Val Val Phe Gly
 625 630 635

GGG AGA CAA CAA GTA GAA ACA ACC AAA TAATGGAATA CTAAATATGA
 Ala Arg Gln Gln Val Glu Thr Thr Lys
 640 645

CTAAAAAGC TTCTAGAGC CGAATTC

FIG.9 A.

GAATTCGGCT TCGATCCAT ATG AAA TCT GTA CCT CTT ATC TCT GGT GGA CTT
 Met Lys Ser Val Pro Leu Ile Ser Gly Gly Leu
 1 5 10

TCC TTT TTA CTA AGT GCT TGT AGC GGA GGG TCT TTT GAT GTA GAT
 Ser Phe Leu Leu Ser Ala Cys Ser Gly Gly Ser Phe Asp Val Asp
 15 20 25

AAC GTC TCT AAT OCA TCC TCT TCT AAA CCA CGT TAT CAA GAC GAT ACT
 Asn Val Ser Asn Pro Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr
 30 35 40

TCA AGT TCA ACA ACA AAA TCT AAT TTG AAA AAG TTG TCC ATT CCT TCT
 Ser Ser Ser Arg Thr Lys Ser Asn Leu Lys Lys Leu Ser Ile Pro Ser
 45 50 55

TTA GGG GGA GGG ATG AAG TTA GTG GCT CAG AAT CTT AGT GAT AAG AAC
 Leu Gly Gly Gly Met Lys Leu Val Ala Gln Asn Leu Ser Asp Lys Asn
 60 65 70 75

AAA CCT AGT CTC TTA AAT GAA GAT GAC TAT ATA TCA TAT TTT TCC TCA
 Lys Pro Ser Leu Leu Asn Glu Asp Tyr Ile Ser Tyr Phe Ser Ser
 80 85 90

FIG.9B.

CIT TCT ACA ATT CAA CAT GAT GTT AAA AAA GAA AAT AAA CGC CAT ACA
 Leu Ser Thr Ile Gln Asp Asp Val Lys Lys Glu Asn Lys Arg His Thr
 95 100 105

AAT CCA GTT GGC TCA ATA GAC GAG CCT AAC GCA ACA AAT CCA CCC GAA
 Asn Pro Val Gly Ser Ile Asp Glu Pro Asn Ala Thr Asn Pro Pro Glu
 110 115 120

AAG CAT CAT GCA CAA AGA TAT GTA TAT TCA GGG CTT TAT TAT ATT CCA
 Lys His His Gly Gln Arg Tyr Val Tyr Ser Gly Leu Tyr Tyr Ile Pro
 125 130 135

TCG TGG AGT CAT TCC TCA AAT GGC AAG CTT TAT TTA GGT TAC TAT GGA
 Ser Trp Ser His Ser Ser Asn Gly Lys Leu Tyr Leu Gly Tyr Tyr Gly
 140 145 150 155

TAT GCG TTT TAT TAT GGT AAT AAA ACT GCA ACA AAC TTG CCA GTA AGC
 Tyr Ala Phe Tyr Tyr Gly Asn Lys Thr Ala Thr Asn Leu Pro Val Ser
 160 165 170

GGC ATA GCT AAA TAC AAA GGA ACT TGG GAT TTT ATT ACT GCA ACT AAA
 Gly Ile Ala Lys Tyr Lys Gly Thr Trp Asp Phe Ile Thr Ala Thr Lys
 175 180 185

FIG.9C.

AAT GGC CAA GGT TAT TCT TTA TTT GGT AGC GCT TTT GGA GCT TAT AAT
 Asn Gly Gln Arg Tyr Ser Leu Phe Gly Ser Ala Phe Gly Ala Tyr Asn
 190 195 200

AGA GCG AGT GGT ATT TCA GAA GAT ATA GAT AAT TTA GAA AAT AAT CTA
 Arg Arg Ser Ala Ile Ser Glu Asp Ile Asp Asn Leu Glu Asn Asn Leu
 205 210 215

AAG AAT GGT GCG GGA TTA ACT AGT GAA TTT ACT GTC AAT TTT GGT AGG
 Lys Asn Gly Ala Gly Leu Thr Ser Glu Phe Thr Val Asn Phe Gly Thr
 220 225 230 235

AAA AAG CTC ACT GGA AAA CTT TAT TAT AAT GAA AGG GAA ACA AAT CTT
 Lys Lys Leu Thr Gln Lys Leu Tyr Tyr Asn Glu Arg Glu Thr Asn Leu
 240 245 250

AAT AAA TTA CAA AAG AGA AAA CAT GAA CTC TAT GAT ATA GAT GGC GAT
 Asn Lys Leu Gln Lys Arg Lys His Glu Leu Tyr Asp Ile Asp Ala Asp
 255 260 265

ATT TAT AGT AAT AGA TTC AGA GGT AAA GTA AAG CCA ACA ACC CAA AAA
 Ile Tyr Ser Asn Arg Phe Arg Gly Lys Val Lys Pro Thr Thr Gln Lys
 270 275 280

FIG.9D.

GAT TCT CAA GAA CAT OCC TTT ACC AGC GAG GGA ACA TTA GAA GGT GGT
 Asp Ser Gln Glu His Pro Phe Thr Ser Glu Gly Thr Leu Glu Gly Gly
 285 295
 TTT TAT GGG CCT AAC GGT GAA CAA TTA GGA GGA AAG TTT TTA GCT GGC
 Phe Tyr Gly Pro Asn Gly Glu Glu Leu Gly Gly Lys Phe Leu Ala Gly
 300 305 310 315
 GAT AAC GGA GTT TTT GGG GTA TTT AGT GCC AAA GAA GAA GAA ACA AAA
 Asp Asn Arg Val Phe Gly Val Phe Ser Ala Lys Glu Glu Thr Lys
 320 325 330
 GAC AAA AAA TTA TCC AGA GAA ACC TTA ATT GAT GGC AAG CTA ATT ACT
 Asp Lys Lys Leu Ser Arg Glu Thr Leu Ile Asp Gly Lys Leu Ile Thr
 335 340 345
 TTT AAA AGA ACT GAT GCA ACA ACC AAT ACA GCA GCC AAT GCA AAA ACC
 Phe Lys Arg Thr Asp Ala Thr Thr Asn Thr Ala Ala Asn Ala Lys Thr
 350 355 360
 GAT GAA AAA AAC TTT ACG ACG AAA GAT ATA CCA AGT TTT GGT GAA GCT
 Asp Glu Lys Lys Asn Phe Thr Thr Lys Asp Ile Pro Ser Phe Gly Glu Ala
 365 370 375

FIG.9E.

GAT TAC CTT TTA ATT GAT AAT TAC CCT GGT CTT TTC OCT GAA GAA
 Asp Tyr Leu Leu Ile Asp Asn Tyr Pro Val Pro Leu Phe Pro Glu Glu
 380 385 390 395

AAT ACT AAT GAT TTC ATA ACT AGT AGG CAC CAT AAG GTA GGA GAT AAA
 Asn Thr Asn Asp Phe Ile Thr Ser Arg His His Lys Val Gly Asp Lys
 400 405 410

ACC TAT AAA GTA GAA GCA TGT TGC AAG AAT CTA AGC TAT GTG AAA TTT
 Thr Tyr Lys Val Glu Ala Cys Cys Lys Asn Leu Ser Tyr Val Lys Phe
 415 420 425

GGT ATG TAT TAT GAA GAC CCA TTA AAT GGA GAA AAT GGC AAA GAA AAA
 Gly Met Tyr Tyr Glu Asp Pro Leu Asn Gly Glu Asn Gly Lys Glu Lys
 430 435 440

GAA AAA GAA AAA GAA AAA GAC AAA GAA AAA GCG ACA ACA TCT ATC
 Glu Lys Glu Lys Lys Asp Lys Glu Lys Gln Ala Thr Thr Ser Ile
 445 450 455

AAG ACT TAT TAT CAA TTC TTA TTA GGT CAC CGT ACT GGC AAG GGC GAC
 Lys Thr Tyr Tyr Gln Phe Leu Leu Gly His Arg Thr Ala Lys Ala Asp
 460 465 470 475

FIG.9F.

ATA CCT GCA ACG GGA AAC GTG AAA TAT CCG GGT AAT TGG TTT GGT TAT
 Ile Pro Ala Thr Gly Asn Val Lys Tyr Arg Gly Asn Trp Phe Gly Tyr 485
 490
 ATT GGT GAT GAC AAG ACA TCT TAC TCC ACT ACT GGA GAT AAA AAT GCT
 Ile Gly Asp Asp Lys Thr Ser Tyr Ser Thr Thr Gly Asp Lys Asn Ala 505
 495 500
 GTC GCC GAG TTT GAT GTA AAT TTT GCC GAT AAA ACA TTA ACA GGC ACA
 Val Ala Glu Phe Asp Val Asn Phe Ala Asp Lys Thr Leu Thr Gly Thr 520
 510 515
 TTA AAA CGA CAC GAT AAT GGA AAT CCC GTA TTT ACA ATT AAT GCA AGC
 Leu Lys Arg His Asp Asn Gly Asn Pro Val Phe Thr Ile Asn Ala Ser 535
 525 530
 TTT CAA AGT GGT AAG AAT GAC TTC ACT GGT ACA GCA ACC GCA AAC AAT
 Phe Gln Ser Gly Lys Asn Asp Phe Thr Gly Thr Ala Thr Ala Asn Asn 555
 540 545
 GTA GCG ATT GAT CCC CAA AAT ACA AOC ACA TCT AGA GTC AAT TTC
 Val Ala Ile Asp Pro Gln Asn Thr Thr Thr Ser Arg Val Asn Phe 570
 560 565

FIG.96.

ACG GCA ACA GTA AAC GCG GCA TTT TAT GGA CCT AAG GCT ACA GAA TTA
 Thr Ala Thr Val Asn Gly Ala Phe Tyr Gly Pro Lys Ala Thr Glu Leu
 575 580 585

GCG GGT TAT TTC ACT TAT AAC GGA AAC AAT CCT ACA GAT AAA AAT TTC
 Gly Gly Tyr Phe Thr Tyr Asn Gly Asn Asn Pro Thr Asp Lys Asn Ser
 590 595 600

TCA ACC GTT TCA CCA TCC AAT TCA GCA AAT GCT GGT GCT GCC GTT GIG
 Ser Thr Val Ser Pro Ser Asn Ser Ala Asn Ala Arg Ala Ala Val Val
 605 610 615

TTT GCG GCT AAA AAA CAA GTA GAA ACA ACC AAC AAG TAAACACAC
 Phe Gly Ala Lys Lys Gln Val Glu Thr Thr Asn Lys
 620 625 630

CAAGTAATCG AATTAATAAA ATGACTAATAA AAGCTTCTAG AAAGCGAAT TC

FIG.10A.

ATG AAA TCT GTA CCT CTT ATC TCT GGT GGA CTT TCC CTT TTA TTA AGT
 Met Lys Ser Val Pro Leu Ile Ser Gly Gly Leu Ser Leu Leu Ser
 1 5 10
 GCT TCT AGC GGG GGA GGT GGT TCT TTT GAT GTA GAT GAC GTC TCT AAT
 Ala Cys Ser Gly Gly Gly Ser Phe Asp Val Asp Asp Val Ser Asn
 20 25 30
 CCC TCC TCT TCT AAA CCA CGT TAT CAA GAC GAT ACC TCG AGT CAA AGA
 Pro Ser Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr Ser Ser Gln Arg
 35 40 45
 ACA AAA TCT AAT TTG GAA AAG TTG TCC ATT CCT TCT TTA GGA GGA GGG
 Thr Lys Ser Asn Leu Glu Lys Leu Ser Ile Pro Ser Leu Gly Gly Gly
 50 55 60
 ATG AAA TTG GTG CCT CAG AAT CTG AGT GGT AAT AAA GAA CCT AGT TTC
 Met Lys Leu Val Ala Gln Asn Leu Ser Gly Asn Lys Glu Pro Ser Phe
 65 70 75 80
 TTA AAT GGA AAT GAC TAT ATG ATA TTT TCC TCA CGT TCT ACG ATT AAA
 Leu Asn Gly Asn Asp Tyr Met Ile Phe Ser Ser Arg Ser Thr Ile Lys
 85 90 95

FIG.10B.

GAT GAT GTT GAA AAT AAC AAT ACA AAC GGG GAC TAT ATT GGC TCA
 Asp Asp Val Glu Asn Asn Thr Asn Gly Gly Asp Tyr Ile Gly Ser
 100 105 110

ATA GAC GAG CCT AGT ACA ACA AAT CCA CTC GAA AAG CAT CAT GCA CAA
 Ile Asp Glu Pro Ser Thr Thr Asn Pro Leu Glu Lys His His Gly Gln
 115 120 125

AGG TAT GTA TAT TCA GGG CTT TAT TAT ATT CAA TCG TGG AGT CTA ACA
 Arg Tyr Val Tyr Ser Gly Leu Tyr Tyr Ile Gln Ser Trp Ser Leu Arg
 130 135 140

GAT TTA CCA AAG AAG TTT TAT TCA GGT TAC TAT GGA TAT GCG TAT TAC
 Asp Leu Pro Lys Lys Phe Tyr Ser Gly Tyr Tyr Gly Tyr Ala Tyr Tyr
 145 150 155 160

TTT GGC AAG GAA ACA GCC ACT ACA TTA CCT GTA AAT GGC GAA GCA ACG
 Phe Gly Lys Glu Thr Ala Thr Thr Leu Pro Val Asn Gly Glu Ala Thr
 165 170 175

TAT AAA GGA ACT TGG GAT TTC ATC ACT CCA ACT ACA AAT GGC AAA AGT
 Tyr Lys Gly Thr Thr Asp Phe Ile Thr Ala Thr Arg Asn Gly Lys Ser
 180 185 190

FIG.10C.

TAT TCT TTG TTA AGT AAT AAC CAA GCT TAT TCC AAA CGT AGT CCA
Tyr Ser Leu Ser Asn Asn Arg Gln Ala Tyr Ser Lys Arg Ser Ala
195 200 205

ATT CCA GAA GAC ATT GAT TTA GAA AAT GAT CCA AAG AAT GGT GAG ACG
Ile Pro Glu Asp Ile Asp Leu Glu Asn Asp Pro Lys Asn Gly Glu Thr
210 215 220 225

AGA TTA ACT AGT GAA TTT ACT GTG AAT TTT GGT ACG AAA AAG CTC ACA
Arg Leu Thr Ser Glu Phe Thr Val Asn Phe Gly Thr Lys Lys Leu Thr
225 230 235 240

GGT CGA CTT TAT TAC CAT TTA CGT AAA ACA AAT GCT AAT GAA AAC CAA
Gly Gly Leu Tyr Tyr His Leu Arg Lys Thr Asn Ala Asn Glu Asn Gln
245 250 255

AAT AGA AAA CAT AAA CTC TAC AAT CTA GAA GCT CAT GTG TAT AGC AAC
Asn Arg Lys His Lys Leu Tyr Asn Leu Glu Ala Asp Val Tyr Ser Asn
260 265 270

CGA TTC AGA GGT AAA GTA AAG CCA ACC AAA GAG TCT TCT GAA GAA CAT
Arg Phe Arg Gly Lys Val Lys Pro Thr Lys Glu Ser Ser Glu Glu His
275 280 285

FIG.10D.

CCC TTT ACC ACC GAG GGA ACA TTA GAA GGT GGT TTT TAT GGG CCT AAT
 Pro Phe Thr Ser Glu Gly Thr Leu Glu Gly Phe Tyr Gly Pro Asn
 290 300

 GGT GAA GAA CTA GGG GGA AAA TTT TTA GCT ACC GAT AAA AAA GTT TTT
 Ala Glu Glu Leu Gly Gly Lys Phe Leu Ala Ser Asp Lys Lys Val Phe
 305 310 315 320

 GGG GTA TTT AGT GCC AAA GAA CAG CAA GAA ACG GAA GAA AAC AAA AAA
 Gly Val Phe Ser Ala Lys Glu Gln Gln Thr Glu Glu Asn Lys Lys
 325 330 335

 TTA CTC AAA GAA ACC TTA ATT GAT GGC AAG CTA ACT ACT TTC TCT ACT
 Leu Leu Lys Glu Thr Leu Ile Asp Gly Lys Leu Thr Thr Phe Ser Thr
 340 345 350

 AAA AAA ACC AAT GCA ACA ACC GAT GCA ACA ACC AGT ACA ACA ACC AGT
 Lys Lys Thr Asn Ala Thr Thr Asp Ala Thr Thr Ser Thr Thr Ser
 355 360 365

 ACA GCA ACC AAT GCA ACA GCC GAT GCA GAA AAC TTT ACG ACA AAA GAT
 Thr Ala Thr Asn Ala Thr Ala Asp Ala Glu Asn Phe Thr Thr Lys Asp
 370 375 380

FIG.10E.

ATA TCA AGT TTT GGT GAA GCT GAT TAT CTT TTA ATT GAT AAT TAC CCT	
Ile Ser Ser Phe Gly Glu Ala Asp Tyr Leu Ile Asp Asn Tyr Pro	395 400
385	
GGT CCT CTT TTA CTT GAA AAT ACT AAT GAT TTC ATA AGC AGT AAG CAC	
Val Pro Leu Leu Pro Glu Asn Thr Asn Asp Phe Ile Ser Ser Lys His	405 410 415
CAT GAG GTA GGA GGT AAA CAC TAT AAA GTG GAA GCA TGT TGC AAG AAT	
His Glu Val Gly Gly Lys His Tyr Lys Val Glu Ala Cys Cys Lys Asn	420 425 430
CTA AGC TAT GTG AAA TTT GGT ATA TAT TAT GAG GAT AAT GAG AAG AAC	
Leu Ser Tyr Val Lys Phe Gly Ile Tyr Tyr Glu Asp Asn Glu Lys Asn	435 440 445
ACC AAA ATT GAA ACA GAA CAA TAC CAC CAA TTT TTG TTA GGT CTC CGT	
Thr Lys Ile Glu Thr Glu Gln Tyr His Gln Phe Leu Leu Gly Leu Arg	450 455 460
ACT CCC AGT TCT CAA ATT CCT GCA ACG GGA AAC GTG AAA TAT CGC GGT	
Thr Pro Ser Ser Gln Ile Pro Ala Thr Gly Asn Val Lys Tyr Arg Gly	465 470 475 480

FIG.10F.

AGT TCG TTT GGT TAT ATT GGT GAT GAC AAG ACA TCT TAC TCC ACT ACT
Ser Trp Phe Gly Tyr Ile Gly Asp Asp Lys Thr Ser Tyr Ser Thr Thr
485 490 495

GCA GAT AAA AAT GGT CTC GCC GAG TTT GAT GTA AAT TTT ACC GAT AAA
Gly Asp Lys Asn Ala Leu Ala Glu Phe Asp Val Asn Phe Thr Asp Lys
500 505 510

AAG CTA ACA GGC GAA TTA AAA CGA GCC GAT AAT CAA AAT ACC GTA TTT
Lys Leu Thr Gly Glu Leu Lys Arg Ala Asp Asn Gln Asn Thr Val Phe
515 520 525

ACA ATT AAT GCA GAC TTT AAA AAT AAT GAT AAT GCC TTC AAA GGT ACA
Arg Ile Asn Ala Asp Phe Lys Asn Asn Asp Asn Ala Phe Lys Gly Thr
530 535 540

GCA ACC GCA GAA AAT TTT GTA ATA GAT GGT AAC AAT AGT CAA ACT CGA
Ala Thr Ala Glu Asn Phe Val Ile Asp Gly Asn Asn Ser Gln Thr Gly
545 550 555 560

AAT ACC CAA ATT AAT ATT AAA ACT GAA GTA AAT GGG GCA TTT TAT GGT
Asn Thr Gln Ile Asn Ile Lys Thr Glu Val Asn Gly Ala Phe Tyr Gly
565 570 575

FIG.106.

CCG AAC GCT ACA GAA TTA GGC GGT TAT TTC ACT TAT AAC GGA AAA AAT
Pro Asn Ala Thr Glu Leu Gly Tyr Phe Thr Asn Gly Lys Asn
580 585 590

CCT ACA GAT AAA AAT TCT GAA AGT TCC TCA ACC GTA CCT TCA CCA CCC
Pro Thr Asp Lys Asn Ser Glu Ser Ser Thr Val Pro Ser Pro Pro
595 600 605

AAT TCA CCA AAT GCA AGA GCT GCA GTT GTC TTT GGT GCT AAA AAA CAA
Asn Ser Pro Asn Ala Arg Ala Ala Val Phe Gly Ala Lys Lys Gln
610 615 620

GTA GAA AAA AAC AAC AAG TAAACACAC CAGTATATGG AATACTAAAA
Val Glu Lys Asn Asn Lys
625 630

ATGACTAAAA AACCTTCTTAG AAGCGAATT C

FIG.11A.

ATG AAA TCT GTA CCT CTT ATC TCT GGT GGA CTT TOC TTT TTA CTA AGT
 Met Lys Ser Val Pro Leu Ile Ser Gly Gly Leu Ser Phe Leu Leu Ser
 1 5 10
 GCT TGT AGC GGA GGG GGG TCT TTT GAT GTA GAT AAC GTC TCT TAT AAC ACC
 Ala Cys Ser Gly Gly Gly Ser Phe Asp Val Asp Asn Val Ser Asn Thr
 20 25 30
 CCC TCT TCT AAA CCA CGT TAT CAA GAC GAT ACC TOG AAT CAA AGA ACA
 Pro Ser Ser Lys Pro Arg Tyr Gln Asp Thr Ser Asn Gln Arg Thr
 35 40 45
 AAA TCT AAA TTG CAA AAG TTG TOC ATT CCT TCT TTA GGA GGA GGG ATG
 Lys Ser Lys Leu Glu Lys Leu Ser Ile Pro Ser Leu Gly Gly Gly Met
 50 55 60
 AAG TTA GTT GTG CAA AAT TTT GCT GGT GCT AAA GAA OCT AGT TTC TTA
 Lys Leu Val Val Gln Asn Phe Ala Gly Ala Lys Glu Pro Ser Phe Leu
 65 70 75 80
 AAT GAA AAT GAC TAT ATA TCA TAT TTT TOC TCA CTT TCT ATG ATT AAA
 Asn Glu Asn Asp Tyr Ile Ser Tyr Phe Ser Ser Leu Ser Met Ile Lys
 85 90 95

FIG.11B.

CAT CAT GTT GAA AAT AAC AAT AAA AAT AAG GAT ACT CCA ATT GGC TCA
 Asp Asp Val Glu Asn Asn Lys Asn Lys Asp Thr Pro Ile Gly Ser
 100 105 110

ATA GAC GAG CTT AGA GCA CCA AAT TCA AAC GAA AAT CAT CAA AAT CAT
 Ile Asp Glu Pro Arg Ala Pro Asn Ser Asn Glu Asn His Gln Asn His
 115 120 125

CAT GCA CAG CAA TAT GTA TAT TCG GGT CTT TAT TAT ATT CCA TCG TGG
 His Gly Gln Gln Tyr Val Tyr Ser Gly Leu Tyr Tyr Ile Pro Ser Trp
 130 135 140

CGT CTA ATA AAT TTA CCA AAT AAG TTT TAT TCA GGT TAC TAT GCA TAT
 Arg Leu Ile Asn Leu Pro Asn Lys Phe Tyr Ser Gly Tyr Tyr Gly Tyr
 145 150 155 160

GCG TAT TAC TTT GGC AAG CAA ACT GCC ACT ACA TTA CCT GTA AAT GGC
 Ala Tyr Tyr Phe Gly Lys Gln Thr Ala Thr Thr Leu Pro Val Asn Gly
 165 170 175

GAA GCA ACG TAT AAA GCA ACT TGG AGC TTC ATC ACC GCA ACT GAA AGA
 Glu Ala Thr Tyr Lys Gly Thr Trp Ser Phe Ile Thr Ala Thr Glu Arg
 180 185 190

FIG.11C.

GCC AAA AAT TAT TCT TTG TTC AAT AAT ACA GGT CAA GCT TAT TCT CGA
Gly Lys Asn Tyr Ser Leu Phe Asn Asn Arg Gly Gln Ala Tyr Ser Arg
195 200 205

CGT AGT GCT ACT CCA GGA GAT ATT GAT TTA GAA AAC GGT GAC GCA GGC
Arg Ser Ala Thr Pro Gly Asp Ile Asp Leu Glu Asn Gly Asp Ala Gly
210 215 220

TTA ACA AGT GAA TTT ACT GTC AAT TTT CGT ACA AAA AAG CTC ACT CGA
Leu Thr Ser Glu Phe Thr Val Asn Phe Gly Thr Lys Lys Leu Thr Gly
225 230 235 240

GAA CCT TAT TAT AAT GAA AGG GAA ACA AAT CTT AAT CAA TCA AAA GAT
Glu Pro Tyr Tyr Asn Glu Arg Glu Thr Asn Leu Asn Gln Ser Lys Asp
245 250 255

AGA AAA CAT AAA CTC TAC GAT CTA GAA GCT GAT GTG TAT AGC AAC CGA
Arg Lys His Lys Leu Tyr Asp Leu Glu Ala Asp Val Tyr Ser Asn Arg
260 265 270

TTC ACA GGT ACA GTA AAG CCA ACC AAA AAA GAG TCT TCT GAA GAA CAT
Phe Arg Gly Thr Val Lys Pro Thr Lys Lys Glu Ser Ser Glu Glu His
275 280 285

FIG.11D.

CCC TTT ACC ACC GAG GGA ACA TTA GAA GGT GGT TTT TAT GGG CCT AAT	
Pro Phe Thr Ser Glu Gly Thr Leu Glu Gly Phe Tyr Gly Pro Asn	290
	295
GCT GAA GAA CTA GGG GGA AAA TTT TTA GCT ACC GAT AAA AAA GTT TTT	
Ala Glu Glu Leu Gly Gly Lys Phe Leu Ala Ser Asp Lys Lys Val Phe	300
	305
	310
	315
GGG GTA TTT ACT GCC AAA GAA AAG GAA AAA CCA AAA TTA CCC AAA	
Gly Val Phe Ser Ala Lys Glu Thr Glu Glu Lys Pro Lys Leu Pro Lys	320
	325
	330
	335
GAA ACC TTA ATT GAT GGC AAG CTA ACT ACT TTC TCT AAA ACA ACC GAT	
Glu Thr Leu Ile Asp Gly Lys Leu Thr Thr Phe Ser Lys Thr Thr Asp	340
	345
	350
ACA ACA ACC AAT AAA ACA ACC AGT GCA AAA ACC AAT ACA GAA AAC TTT	
Thr Thr Thr Asn Lys Thr Thr Ser Ala Lys Thr Asn Thr Glu Asn Phe	355
	360
	365
ACG ACA AAA GAT ATA CCA AGT TTT GGT GAA GCT GAT TAT CTT TTA ATT	
Thr Thr Lys Asp Ile Pro Ser Phe Gly Glu Ala Asp Tyr Leu Leu Ile	370
	375
	380

FIG.11E.

GAT AAT TAC CCT ATT CCG CTT TTA CCT GAG AGT GGT GAT TTC ATA AGT
 Asp Asn Tyr Pro Ile Pro Leu Leu Pro Glu Ser Gly Asp Phe Ile Ser
 385 390 395 400
 AGT AAG CAC CAT GAG GTA GGA GGT AAA CGC TAT AAA GTG GAA GCA TGT
 Ser Lys His His Glu Val Gly Gly Lys Arg Tyr Lys Val Glu Ala Cys
 405 410 415
 TGC AAG AAT CTA TGC TAT GTG AAA TTT GGT ATG ATG TAT TAT GAG GAT AAA
 Cys Lys Asn Leu Cys Tyr Val Lys Phe Gly Met Tyr Tyr Glu Asp Lys
 420 425 430
 GAG AAC AAC AAA AAT GAA ACA GAC AAA GAA AAA GAA CAA ACG ACA
 Glu Asn Asn Lys Asn Glu Thr Asp Lys Glu Lys Glu Lys Gln Thr Thr
 435 440 445
 ACA TCT ATC AAG ACT TAT TAT CAA TTC TTA TTA GGT CTC CGG ACT CCC
 Thr Ser Ile Lys Thr Tyr Tyr Gln Phe Leu Leu Gly Leu Arg Thr Pro
 450 455 460
 AGT TCT GAA ATT CCT AAA ATG GGA AAC GTG ACA TAT CGC GGT AGT TGG
 Ser Ser Glu Ile Pro Lys Met Gly Asn Val Thr Tyr Arg Gly Ser Thr
 465 470 475 480

FIG.11F.

TTT GGT TAT ATT GGT GAT GAC AAG ACA TCT TAC TCC GCT ACA GCA GAT
 Phe Gly Tyr Ile Gly Asp Lys Thr Ser Tyr Ser Ala Thr Gly Asp
 485 490 495

AAA CGA CAA GAT AAA AAT GCT CCC GAG TTT AAT GCT GAT TTT AAC
 Lys Arg Gln Asp Lys Asn Ala Pro Ala Glu Phe Asn Ala Asp Phe Asn
 500 505 510

AAT AAA AAG CTA ACA GGC ACA TCA AAA CGA CAC GAT AAT CAA AAT CCC
 Asn Lys Lys Leu Thr Gly Thr Ser Lys Arg His Asp Asn Gln Asn Pro
 515 520 525

GTG TTT AAC ATT AAG GCA ACC TTT CAA AAT GGT CGG AAT GAC TTT GAA
 Val Phe Asn Ile Lys Ala Thr Phe Gln Asn Gly Arg Asn Asp Phe Glu
 530 535 540

GGT ACA GCA ACC GCA GAA AAT TTT GTA ATA GAT GGT AAA GAT ACT CAA
 Gly Thr Ala Thr Ala Glu Asn Phe Val Ile Asp Gly Lys Asp Ser Gln
 545 550 555 560

GCA AAT ACC CCA ATT AAT ATT ACA ACT AAA GTA AAC GGG GCA TTT TAT
 Gly Asn Thr Pro Ile Asn Ile Thr Thr Lys Val Asn Gly Ala Phe Tyr
 565 570 575

FIG.11G.

CGA CCT GAT GCT TCT GAA TTA GGC GGT TAT TTC ACC TAT AAC GGA AAA	
Gly Pro Asp Ala Ser Glu Leu Gly Tyr Phe Thr Tyr Asn Gly Lys	580
	585
GAC ACT ATA ACT AAA AAT ACT GAA AGT TCC TCA ACC GTA CCT TCA CCA	
Asp Thr Ile Thr Lys Asn Thr Glu Ser Ser Thr Val Pro Ser Pro	595
	600
CCC AAT TCA CCA AAT GCA AGA GCT GCA GTT GIG TTT GGA GCT AAA AAA	
Pro Asn Ser Pro Asn Ala Arg Ala Ala Val Val Phe Gly Ala Lys Lys	610
	615
CAA GTA GAA ACA AOC AAC TAGAAAAAA CAAATATATCG AATACTAAAA	
Gln Val Glu Thr Thr Asn Lys	620
	625
ATGACTAAAA AACCTCTCTAG AAGCCGAT TC	

[illegible]

...5' GGATCCAT
... \ATGAATCTGTACCTCTTATCTCTGGT 3'

..... M K S V P L I S G
TATAAATCTATGAAATCTGTACCTCTTATCTCTGTT
TATAAATCTATGAAATCTGTACCTCTTATCTCTGTT
TAT-TAATCTATGAAATCTGTACCTCTTATCTCTGTT
AATATAATCTATGAAATCTGTACCTCTTATCTCTGTT
 EAGAN
 MINNA
 PAK
 SB33

FIG.12B

3' tbp2

5' tbp I

M T K K

GTAGAAACAACCAATAA-----TGGAACTACTAAAAATGACTAAAAAACCCCTATTTTCGCCTAAGT EAGAN
 GTAGAAACAACCAATAA-----TGGAACTACTAAAAATGACTAAAAAACCCCTATTTTCGCCTAAGT MINNA
 GTAGAAACAACCAAGTAA-----TGGAACTACTAAAAATGACTAAAAAACCCCTATTTTCGCCTAAGT DL63
 GTAGAAACAACCAAGTAAAAACAACCAAGTAAATGGAACTACTAAAAATGACTAAAAAACCCCTATTTTCGCCTAAGT PAK

3' TACCTTATGATTTTACTGATTTTT

\CGAAGATCI 5'

M T K K

GTAGAAACAACCAATAA-----TGGAACTACTAAAAATGACTAAAAAA SB12
 GTAGAAACAACCAAGTAAAAACAACCAAGTAATGGAACTACTAAAAATGACTAAAAAA SB29
 GTAGAAAAAACAACCTAGTAAAAACAACCAAGTAATGGAACTACTAAAAATGACTAAAAAA SB30
 GTAGAAACAACCAAGTAAAAACAACCAAGTAATGGAACTACTAAAAATGACTAAAAAA SB32

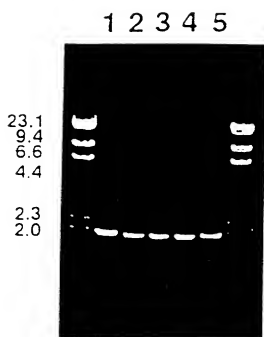


FIG.13.

FIG.14 A.

Comparison of TBP1 amino acid sequences

MTKKPYFRLSIICLLISCVKAEQSIKDTKEALISSEVDQTSTEDSELETISVTAEKIRDKDNEVTGLGKIITSEISREQLNIRDLTRYDPGISV
V.....

 .QQQHL..N.L..SLMTALPVAENTQAGQAEQKQ-----D.Q.K.K.QKT.R.....LV.S.DTL.K.....A.
 .QQQHL..N.L..SLMTALP.VAENTQAGQAEQKQ-----D.Q.K.K.QKT.R.....LV.ADTL.K....D.....A.
 .QQQHL..N.L..SLMTALP.VAENTQAGQAEQKQ-----D.Q.K.K.QKT.R.....LV.ADTL.K....D.....A.

EAGAN
 DL63
 PAK
 SB33
 B16B
 M982
 FA19

VEQGRGASSGYSTRGMDNRNVRALLVDGLPQTQSYVVOPLVARSGYSGTGAINIEYENKAVEISKGSSSEYGNALAGSVTFQSKAADILEGDKSW

K..S.T...VS.I...TA.AA.GGTRTAGSS.....SN.....A..T.T...IGEG.Q.
K..S.T...A.I...TA.AA.GGTRTAGSS.....SN.V.Q.S.....A..T.T.D.VIGEGRQ.
K..S.T...A.I...TA.AA.GGTRTAGSS.....SN.V.Q.S.....A..T.T.D.VIGEGRQ.

EAGAN
 DL63
 PAK
 SB33
 B16B
 M982
 FA19

GIQTKNAYSSKNKGFTHSIAGKGGFEGALITYTORNSETQVHKDALKGVQSDRLIATTDKSSGYFVIQ-----ECPNGDDK--CAA--KPPATLS
V...H.....F...EDQ.A..M.D-----LD.Y...--KTSP.R.....
D.V.....H...KPEDQ.A..M.D-----KP..YNS.LPFA.R..I..
V.....E.....E.F.....KV,
S.T..G.DHAL.Q..L..RS..A.A.L..K.RGR.IHA..G.....FN.VLDE..KE.GSQRYFIVEE..H..YAA--KNKL.ED.SVK
S.T..G..R.L.Q.I.L..RI..A.A.L.H.K.RGG.IRA.E..GR...FN.VLVE-----SSEYAYFIVED..EGKNYET--KSPK.KDVVGK
S.T..G..R.L.Q.I.L..RI..A.A.L.H.K.RGG.IRA.EA.GR...FN.APVD-----GSKYAYFIVEE..K..CHEK--K.NP.KDVVE

EAGAN
 DL63
 PAK
 SB33
 B16B
 M982
 FA19

FIG.14B.

TOSTVSYDVTGANRKPNPKYBSQSWFLRGYHSE-QHYIGIGFEFTQOKFDIRDTFPAYLSPTEIRDSSRSFYPMQDHGAYQHIEDGR-----	EAGAN
S.R.....R.....DK.LQ.P.K.Y.....G.....	DL63
S.R.....RS.K.....K.Y.....R.....	PAK
P.....RS.K.....RTGP.....K.Y.....R.....	SB33
DERK...TQ...S.ILA.LE.G...LF.P.W.LDN-R.V.AVL.R...T...V...FTSEDPV-----GSLKGLGKYSGDNKAE.LFVQG	B16B6
DERQ...TR...P.FLAD.LS...R.LF.P.FR.ENKRR...L.H...T...V.F.TKAVFDAN.KQAGSLPGNKYAGNHKY.GLFTNG	M982
DERQ...TR...P.FLAD.LS...R.LF.P.FR.ENKRR...L.H...T...V.F.TKAVFDANQKAGSLPGNKYAGNHKY.GLFTSG	FA19
-----GVKYASGLYFDEHHRQVRGIEVIYENKNKAGIIDKAVLSAQOONILDSYMRTHCSLYPNPSKNCRPTLDKPYYSRDRNVYKKNMLQL	EAGAN
-----N.....Q.....H.....	DL63
-----N.....R.....H.....	PAK
EGSTLQ.IG.GT.VFY..R.T.N.Y.V.V.H.AD.DTWA.Y.R.YDR.G.D.NRLQQ...HDGSD-...DGN...F.K...MI.E.SR.LF.A	SB33
ENGALV.AE.GT.VFY..T.T.S.Y.L.V.T.AD.DTWA.Y.R.YDR.G.D.NHPOQ...ADGSD-.Y..SA..F..K...VI.G.S.RL..A	M982
ENNAIPV.AE.GT.VFY..T.T.S.Y.L.V.T.AD.DTWA.Y.R.YDR.G.D.NHPOQ...ADG-..Y..SA..F..K...VI.G.S.KL..A	FA19
NLEKKIQONMLTHQIVFNLGFDFTSALQHKDYLTRRVATADSIPIKPGETGKPRNGLOQ-PYLYPKPEPFAGQDHCHVQSGSSNYRDCVKRLIKG	EAGAN
.....A.....S..SE.R..A-R.....S.....T.KAELV.G.L.....K.....S.....	DL63
.....T...K..SE.AN--R...YEK..-...TWG.VV...D.K.N.....	PAK
.....T...NI.SGVA--R...YEK..-...S.KVG.V.....K.....S.....	SB33
VFK.AFTAKIR.NLSI...Y.R.K.Q.S.S.YLQNAQV.L.TP.KPFPF---SKDN-..RVSTGKTWTNTP.I.RFGNNT--Y..TP.N.G.N	B16B6
AFK.SFTAKIR.NLSV...R.D.N.R.Q..YQHARAYS.KTPPKTAMP---DK.K-..WVSGGNVVTQOI.LFGNNT--Y..TP.S.N..	M982
AFK.SFTAKIR.NLSV...Y.R.G.N.R.Q..YYQSANRAYS.LKTPQNNKG.TSPNGREKN..WVSGGNVVTQOI.LFGNNT--Y..TP.S.N..	FA19
NYFAARNMALGKYVDLGLGIRYDVSTKANESTISVGKFNFSWNVICVTKPEWLDLSYRLSTGFRNPFSEMYGWRVGGKNDEYVYKPKPETSIN	EAGAN
.....M.....A.....A.....D.TD..I.....	DL63
.....N.S.....	PAK

FIG.14C.

.....I.....A.....N.SD.....	SB33
G..A.VQD.VR..RWA.V.A..	YRS.HSEKSV.T.THR.L..A.V.L..FT.M.T.A..L..A.....A.---	ESLKYLDL...K.F.	B16B6
G..A.V.D.VR..RWA.V.A.L..	YRS.HSDGVS.T.THRTL..A..L..AD..T.A..L..A.....S.---	VQSKAV.ID..K.F.	M982
S..A.V.D.VR..RWA.V.A.L..	YRS.HSDGVS.T.THRTL..A..L..AD..T.A..L..A.....S.---	KIKAV.ID..K.F.	FA19
QERGLAKGDFGNIIEISHFSNAYNLIATAEELSUNG-TGKGNY--GYHNAQNAKLGVNITPAQLDFNGLMKRIPYGMVATFAYNOVKVKQKINAGLAST.....R.....	EAGAN
.....N.....A.....R.....	DL63
.....T.....R.....R.....	PAK
R.A.IVF.....L.A.Y.N..D...GY.TRTQNGQTSASGDP..R.....RIA.I..LGKI.WH.V.GGL.D.L.S.L..RI...	AD.R.DRTF		SB33
K.A.IVF.....L.A.W.N..D..VRGY.AQIKNGKEAKGDP.A.L..S.RIT.I..LGKI.W.V.DKL.E..S.....R.H.R.I.KR.DRTD			B16B6
K.A.IVF.....L.A.W.N..D..VRGY.AQIKGQEVKGNPA.L..S.RIT.I..LGKI.W.V.DKL.E..S.....R.R.R.I.KR.DRTD			M982
			FA19
VSSYLFDAIQPSRVIIIGLYGHPHSNTWGINTMFTQSKAKSONELLGKRALGNNRD-VKSTRKLTRAWHILDVSGYMANKNIMLELGIYNLFNRYVTWK.....N.....	EAGAN
.....Q.....N.....V.RS.LF...V..L.....	DL63
.....V.....Q.....N.....	PAK
T.....VL.....DGI.....Y...VD...SQ..L.GNANAK.AASRR..P.YVT.....NIK.HLT..A.V..L.....			SB33
IQ.H.....VV.....Q.EGK..V.G.L.Y...EIT...S...L.GNSRNT.A.ARR..P.Y.V.....TIK.HFT..A.V..L.....			B16B6
IQ.H.....VV.S...Q.EGK..V.G.L.Y...EIT...S...L.GNSRNT.A.ARR..P.Y.V.....TVK.HFT..A.V..L.H.....			M982
			FA19
EAVRQTAQAVNQHVGSYTRYAASGRNYTLEMKF*	EAGAN		
.....N.....	DL63		
.....*	PAK		
.....*	SB33		
N...G...K..V.N...P...FS.....*	B16B6		
N...G...G.K..V.N...P...FS.....*	M982		
N...A...K..V.N...P...FS.....*	FA19		

FIG.15A.

Comparison of TNP2 amino acid sequences

MKSVLISGGLSFLLSACGGG-SFDVDNVSNTPS--SKPRYQDDTS----	WQRKKS-NLKKLPIPSLGGGKKLVAQLNRGNRPFSLNEDDYISYFSS	EAGAN
.....T.....G.....D.....PS.....	---SS.T.-K.E.S.....A.L.FDRNK..L..S.M-I...	DL63
.....G.....D.....PS.....	---T.....D.E.....FI.AR.....G.M-I...	PAK
.....G.....D.....PS.....	---SS.T.-K.EN.S.....DRTK..L..M-I...	SB12
.....L.....D.....PS.....	---SS.T.....S.....FDRNK..L.....	SB19
.....G.....D.....PS.....	---S.T.-E.S.....S.....GN.M-I...	SB30
.....L.....G.....L.S.ETVODMH..K.E.EK.Q.PES.QDV.E.SGAAYGFAVKLPRNAHF.PKYKFKHP.GSM.WKKLO-R	---T.-K.E.S.....V.FA.A.....N.....	SB32
MNNPLVNOAAWVLPV.....L..G..L.S.DT-EAPRA.K..VS.EKPOA.KD---QG-GYGFAWELKRRN-WYPGAEESEVK..S.WEATGLPL..G..L.S.DT-EAPRA.K..VP.KKPEAKD---QG-GYGFAWELKRRN-WYPGAEESEVK..S.WEATGLP	BL6B6
MNNPLVNOAAWVLPV.....L..G..L.S.DT-EAPRA.K..VP.KKPEAKD---QG-GYGFAWELKRRN-WYPGAEESEVK..S.WEATGLPL..G..L.S.DT-EAPRA.K..VP.KKPEAKD---QG-GYGFAWELKRRN-WYPGAEESEVK..S.WEATGLP	M982
MHFKLNPYALAFSL..-V.....KG...LED.RPNKTTGVSKKEEK.VETAKKEQ---GE.ME.A.YVV.V---V.....KG...LED.RPNKTTGVSKKEEK.VETAKKEQ---GE.ME.A.YVV.V---	FA19
MHFKLNPYALAFSL..-V.....KG...LED.RPNQTAKEAKATTSYQDEETKKKT--EE.D.ME.A.YET---I..R..A.KTETGKRNREV---V.....KG...LED.RPNQTAKEAKATTSYQDEETKKKT--EE.D.ME.A.YET---I..R..A.KTETGKRNREV---	AP205
AP37		
L--STIEKDVK--DNKNKGADLIGSIDEFTNPPEK--HHGQF-----YVYSGLYTPSWLSNDSKN-KF-----YLGYYGYAFY		EAGAN
R-----E...--ND.Q..EHP.D.VD.RAP.SM.N-R-----IQ...R.LP.K-----S.....Y.		DL63
.....E.EKVN.....GR.....E.NG.SQNSN--S..E-----ID..RDYKKEQ.A-----T.....		PAK
.....KA.EK--E.HYTSPV.....K.N--D.R-----I..N..L.N.Y-----Y.S.....Y.		SB12
.....QD..K--E..RHTNPV.....NA.....L.....I.....HSSNGKL-----		SB29
R-----K.D..E--N.T..G.Y.....L.....Q.....R.LPK-----S.....Y.		SB30
.....M.KD.E--N.....KDP.....RAP.SN.NHQN.....Q.....I.....R.INLP-----S.....Y.		SB32
GEPISTSERDE--L..KRG-----SSE--E.KW.DG-----QSRVGVYTNFT..R.YV.LNK--NNI..I.NIV--LFGPDG..Y.K.KEPS		BL6B6
TKPKELPKQK.V..VETDCDSIDYSSPY.TR.NHQNGSAGVGN--QPKQATGHEINQ...WF.KHAA.EK.FS.K.I--KSGDDG.IF.H.KEPS		M982
TEPKLPLKQK.V..SEVTNGNSKMTSPY.SQDA.SSH--ANGAN--QPKNEVTDYKKFK..WF.KHAK.EVKNE.GLVSAKRGDDG.IF.H.KEPS		FA19
-----D..VITNGNL.DVYPK.NSSKNYPDI.....KTQDSSLQ..R..YVIDGEH.GSNE-----VY.		AP205
-----VELSED.IT.LYQESVEIIPH.DELNGKTTSDNVYHS---DSKRLDKNRLK..R..YV.DG.FNEIRNDG.HVFKQGD-----VY.		AP37

FIG.15B.

YGNKTATNLPVNGVAKYGTWDFITATKNGKRYPLLSNGS--HAYYRRSAIPEDIDLENDSKNGDI-GLISEFSADFTKKTGLTGOLSVYTKRKT-----N	EAGAN
F.T.SA.G.T.S.AE.N.E.R.SGGG-Q.S.T.T.DRKT-----T.TVN.....G.Y.NL.E.DAN---K	DL63
E.E.K.K.....N.E..S.F.SIG-Q.S.....S.YNLENGDA-----V.K.E.E.Y.NE..SVN---E	PAK
F.KQ..T..KVT..S.AE.....Q.F.....VKNDENREK.V.....K.Y.NE.E..Q.....H	SB12
.....S.I.....Q.S.FGSAP--G.N.S.....MLENNKNGA--T.TVN.....K.Y.NE.E..-----N	SB29
F.KE..T..E.T.....R.S.S..NR--Q.SK.....P.ETR--T.TVN.....G.Y.HL..NAN---E	SB30
F.KQ..T..E.T.....ER.N.S.FN.RG--Q.S.....T.G.....A--T.TVN.....EY.NE.E.N---L	SB32
KELP-SKITVK.TWD.VTDAMEKORFGL--GSAAGGFKGALSALAEGLVLRNQAEAS--SGHT.F.-MT.EV..SD.TIK.T.YRNN.I.QMNSENKQ	B16B6
RQLPASCKVIYK..WHFVTDTKGQDFREIQRKQKQDVRSGFSGDSEYSNNKNESTLAKDDHEGY--FT.NLEV..N.....K.IRNNASLNNNTNNDK	M982
RQLPASAVIYK..WHFVTDTKGQKFNIDLETSGKGQKYSFGSGDEGETSNRT.SNLAND.HEGY--FT.N.KV.NN.....K.IRNNKVINTRAADG-	FA19
K.SP.KE.....QLLT.T.S..TSNANLNWEGGRNYLN--DD..TKF IGRKRVLSVG.A.PAKH-KYT.Q.EV..A..M..KJ..-D.E.-----	AP205
L.VTPSKE..KKG.IS.....VSNINLEREIDGKDTSGDKNVSATSIETVNR.HKVGE.L.N-EVKGVASHSEFAVDFDNKKLTGSLYRNGYINRK	AP37
NQ--PYEKKLYDIDADIYSNRFRTVKTPEKD-SEHPFTSEGT-LEGGFYCPNAEELGKFLATNDRVFGVSAKETETKKEA-LSKETLIDGLITFFS	EAGAN
S.--NRTH--LE..VH.....K.K.ES.....EQ.....H.KK.L.....QQ..SENKK.P.....T.K	DL63
S.--NTH--TLE.KV.....K.K.KTK--D.....EK.....DPONPENQK..T.....K	PAK
I.--NH.....H.....K.N.Q.-K.....EQ.....G.KK.....G.N.--P.....T..	SB12
NKLOKR.HE.....K..TOKD.Q.....G.....DKK--R.....K	SB29
---NR.H..NLE.V.....K.KES--.....S.KK.....QQ..EENKK.L.....T..	SB30
-SKDR.H..LE..V.....K.....K.ES.....S.KK.....KP.--P.....T..	SB32
IK--TTRYTQATLHGKRFKGCALAAD,GATNG--..I.DSDS.....KG..A..SN..K.AA..G..QKDKKQD.NAAGPA.E-----	B16B6
HT--TOYSLDAQ.TGNRFGTATA.D.KENET-KL--..V.DSSS.S..F..OG..FR..SD.QK.AV.G..TKDKLENG.AA.GS.GAAASGAAG	M982
YT--TEYISLDATLGNRF.GKATA.D..NTGCTKI--..VPDSSS.S..F..OG..FR..SD.GK.AV.G..TKOSTANGNAPAASSG	FA19
IY--TV--NA..RGNRFTGAATASD.NKG-GE.YNF--SADSQS.....K..MA..V.N.KSL.A.....	AP205
A.---VT.R.S.E.AG.....KA.A--AGD---IFTDSNY.....K..MA..FTNNKSL.A.A..-----	AP37
TKKTDKAT-----NATSTAANTTTTNTANTITDEKNFKTEDISSFGADYLLIDKY-----PIPLLPDKNTNDFI	EAGAN
..TNAT.NATT--D.....T.S.K..T.ATANTE..T.K.P.L.....N.....V.F.--ESG...	DL63
RTDATNATT--D.K..ATTA.S--..KK.AE.....P.....GNQ.....E..D..	PAK
..T.....NATA.....AE..K.....N.....V.....-ESG...	SB12

FIG.15C.

.....T-----A..AK.....T.K.P.....N.....V..F.EE.....SB29
N.T-----D-----S..ATNATA,AE..T.K.....N.....V.....E.....SB30
KTTD...NK..TSAK.NTE..T.K.P.....N.....-BSG.....SB32
VID.VRI..GEFEKEQIDSGDKVLVD.VELS.....FOHEFE.....B16B6
S-----SENS--KL..VLD.VEL..LNDKTKLNDJFNSAOLVVD..IMP..PKDSEGNTOADKGNKGTEFTFRKPHNPESDKDAQAGQTNGAQTASN
 PQAATMSET--RL..VLD.VEL..PDGKETKLNDJFNSAATRLVVD..IMP..PT--ESNGQADKGNKGTDFTVTTTYPESDKDKTKAQTGAGGQTASG
 FA19
 -----HNGSNVN.VRIIDASKI..LT..SISELANN..D.SV.I.....GKKIKLAGSG.T
 AP205
 -----SENG--ET..E-----RIIDA.KI.LTQ.NAKELANN..D.SV.I.....GQKI.LAGVN.K
 AP37

SSKHHVTGNKR--YKVEACCSNL5YVKGMYEDPLKEKETETETETETEKDEKEKEKDKERQTAATTNTTYQFLLCHRTPKDDIPK--TGSAKYHGSMFG
K.T--Q.....A.P.--E.K.K.KD.....ATTSIK.....L..SSE.....E.....N.....EAGAN
G.T--K.....KDDDN.NETDKKGGKERT.TTSI.....L..E.....E.....N.....DL63
K.T--Q.K.....V.P.E.....KE.E..ATNLS.....L..SSE.....G.....L.....PAK
 T.R.K.D.T--K.....K.....NG.NG.....E.....ATTSIK.....A.A..A--NV..R.N.....SB12
E.G.H.....K.....I.....N.N.KIE.EQ.H..L..SSQ..A--NV..R.....SB29
E.G.....K.C.....KENKN.T.E.....TTSIK.....L..SSE.....M.NVT..R.....SB30
 -----QNGVRAT--V.....D.MS..KLSKEN--DDM..Q.V..VS.VAARTAN...R.T.Y..B16B6
 TAGTNGKKT.T--E..V.....N.L.Y..LTRKNS--SAMQAGNSQADAKTEQVEQSM..Q.E..DEKE.--TDONVV..R..Y.Y..M982
 TAGVNGQGVGTT..QV.....N.L.Y..LLTREN-----NNSVMQAVKNSS..AD.K.KOIE.SMFLOGERT.ENKIPQEQIV.L.F.Y..FA19
 NKHTIEING.T--MVAV.....E.M..QLW-----QQAEGCKPENNSL..Q.E..AT.KM.--G.NY..I.T.D-
 N..TVEING.T--MVAV.....E.M..QLW-----Q.EGRQOVKNLSL..Q.E..AT.KM.A--G.NY..V.T.D-
 AP37

YITDGTSTSPSGDKKRKNVAEFNVFAEKKLGLGELKRHD7G-NPVFSTIEANFNSSNAFTGTATATN--FVIDGKNSQKNTPINITTKVNGAFYCPKA
S..E..A..E.S.....N..T.....Q--K.N.T.QSGK.D.....KD--LA.....T.GTSKNFTA.-.....EAGAN
S..E..A..E.S.....D.S.N.T.....N..T.K.N.EL.G.-D.....N..TS.AK.....DL63
 LS..S.....EN..L..N.VD.T.KGO.I..NQ--T.T.D.T.KGGK.N.....N.--VA..PQSTQGTNSVNFTA.-.....N..SB12
G.D..TT-----D.N..D.T..T..N--T.N.S.QSGK.D.....N--VA..PQ.T.TTSRVNFTA.-.....N..SB29
G.D..TT-----L..D.N.TD.....A.NQ--T.R.N.D.K.ND..K.....E.....N..TG..Q..K.E.....N..SB30
G.D.....AT..RQ..P.....A.NN..TS.....NQ--N.K.T.Q.GR.D.E.....D..G--SB32

FIG.15D.

..AN--..W.GEASNOEGG.-R...D...ST..IS..T.TAK.RT-S.A.T.T.MIKD--..G.S.V.KTGENG.AL.PQ.TG.SHYTHI-EAT.S.G...KN.
H.AN--..W.GNASD.EGG.-R...T.N..D..I..K.TAENRQ-AQT.T.GWIOG--..G.E...KTAESG.DL.Q...TTRTPKAYITDA..K.G.....
R.AN--..W.GKASNAT.G.-R.K.T.N.DR.EL..T.TAENRS-EAT.T.D.MIEG--..G.K...KTG.DG.AP.QN..TVTHKVIHANA.E.Q.G...N.
AQSVEKNWATA.DD.KSGYRT..D...GN.N.S.K.LFDKN.V...TVD.KIDG--..G..K.KTSDSG.AL.SGS.RYE.VKF.DVA-.S.G....T.
ALVSKG.NWIAEA.NN.ESGYRT..D.N.SD...VN.K.-FDKG.V....TVD.TI.G--..G.I.S.KTSDSG.AL.AGS..HG.AVFSDI-...G....T.
AP37

SELGGYFTYNGN-STATNSESSTVSSSSKNARAAVVFGAR-QQVETT-K*
T.....-----NPTDKN.....EK.....KK.....*
.....KNP.....P.P.P.S.....KF.....N.*
T.....-----PTDK.....P.....*
T.....-----NPTDKN.....P..A.....KK.....N.*
T.....KNP.DK.....P.P.P.....KK.....KNN.*
.....KDTITK.T.....P.P.P.....KK.....N.*
I.M.S.SFP..APEGKOE-----K.S.....KR..LVQ*
E...W.A.P.DKQ.EKAT-----AT..DGNASS.T.....KR..PVQ*
E...W.A.P..EQ.KNA-----E.GNGNSASS.T.....KR.KLVK*
A...Q.HHKSENGSVGA-----K.....KK*
G....Q.HHKSDNGSVGA-----K-R-I.R*

EAGAN
DL63
PAK
SB12
SB29
SB30
SB32
B16B6
M982
FA19
AP205
AP37

B16B6
M982
FA19
AP205
AP37

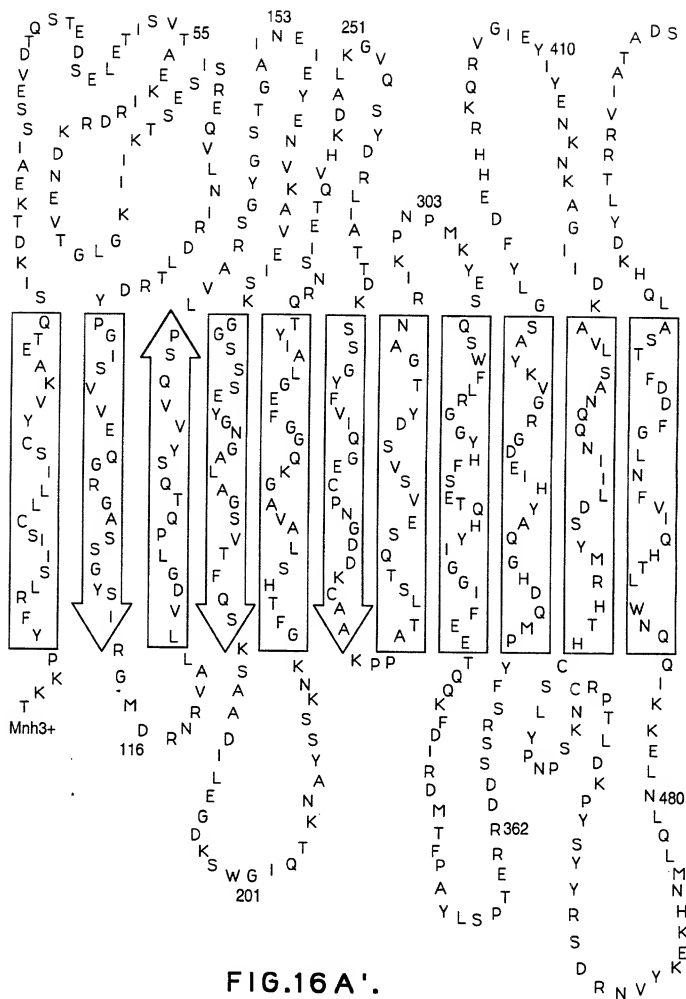
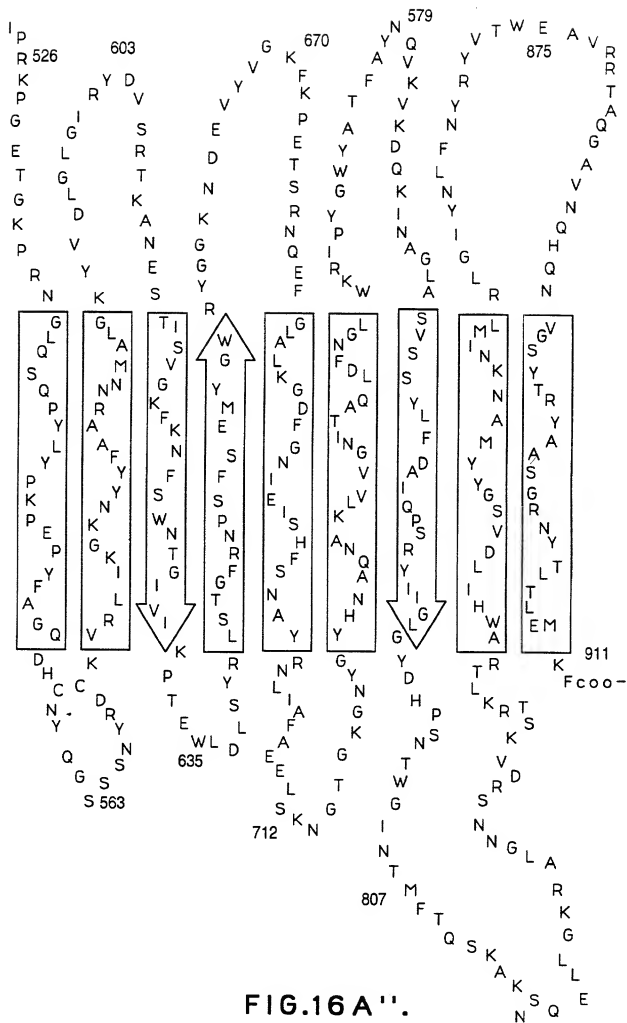


FIG.16A'.



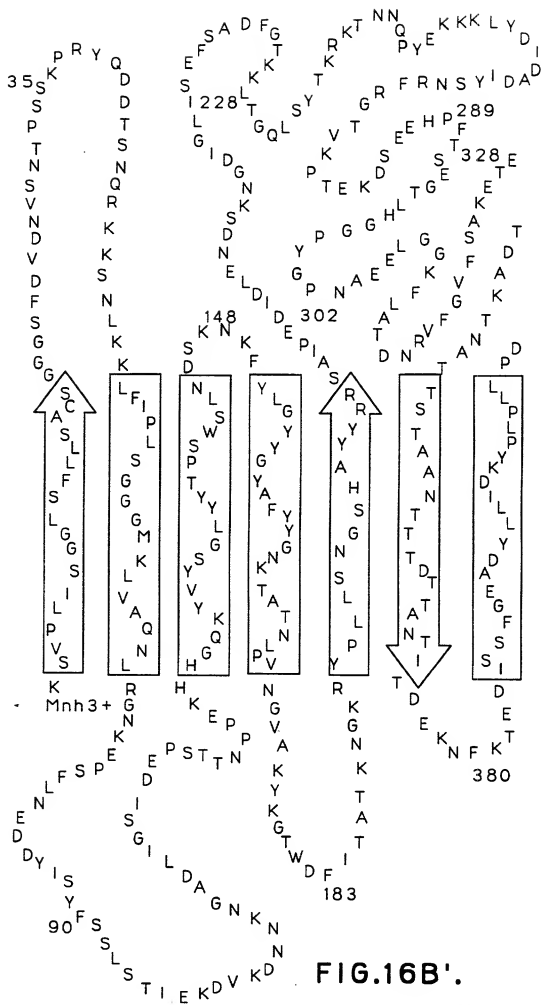


FIG.16B'.

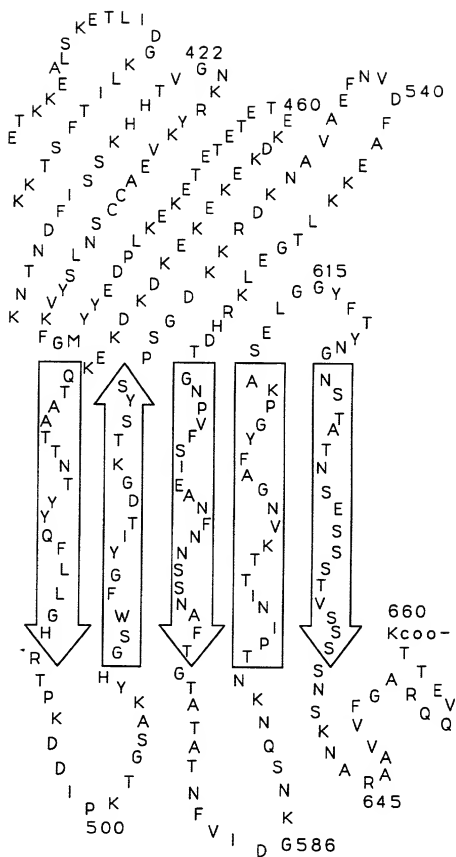


FIG.16B''.

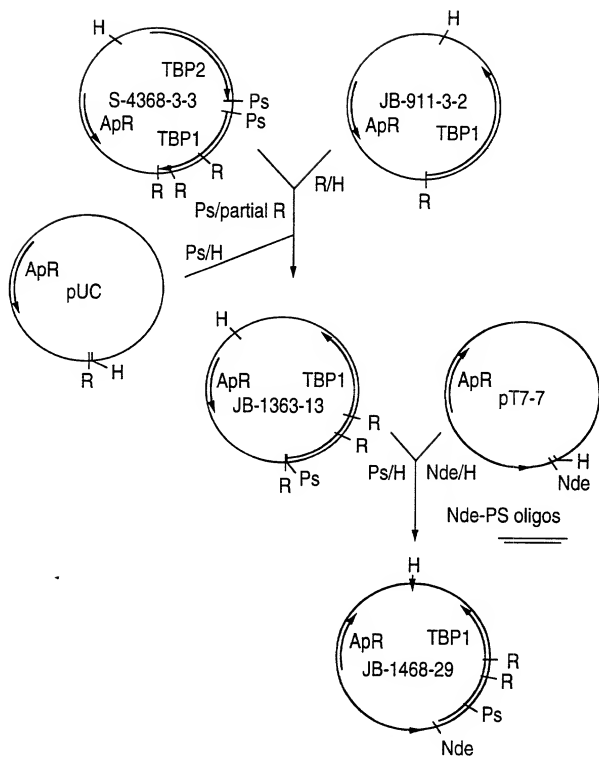


FIG.17.

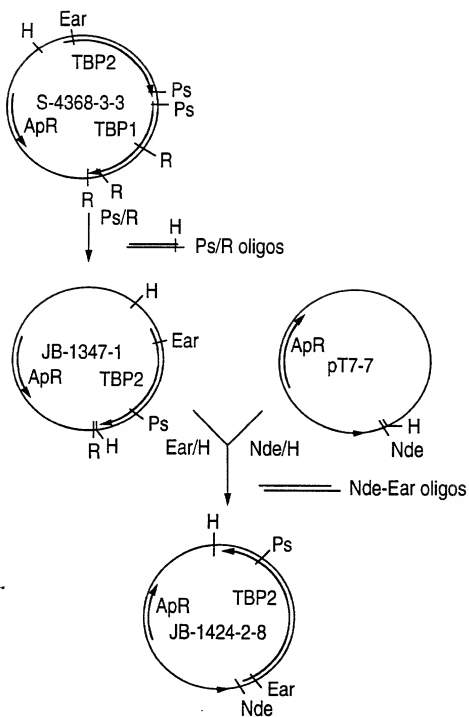


FIG.18

FIG.19. Oligonucleotides to express TBP2 with no signal sequence.

Nde I	Ear I
TATGTGTTCTGGTGGTGTTCCTTTTCGACGTTGACAAACGTTTCTAACACTCCCTCTTCT	
ACACAAGACCAACCACCAAGAAAGCTGCACTGTGCAAGATTGTGAGGGAGAAGATTT	

ATG start codon is underlined
TGT cysteinr of mature protein is double underlined

FIG.20A.

Sequence of oligonucleotide pairs (A, B, C and D) for constructing TBP1 and TBP2 expression plasmids

Oligonucleotide pair A (Seq. ID 86 and 87) to join the T7 promoter and Egan TBP1 gene

Nde I

TATCGAAACTCAAAGTATAAAGATACAAAGAAGCTATATCATCTGAAGT...
ACCTTTGAGTTTCATATTTTCTATCTTTTCTTCGATATAGTAGACTTCA...

Pst I

...GGCACTCAAAGTACAGAAGATTCAGAAATTAGAAACTATCTCAGTCACTGCA
...CCTGTGAGTTTCATCTTCTTAAGTCTTAATCTTTGATAGAGTCAGTG

Oligonucleotide pair B (Seq. ID 88 and 89) to join the T7 promoter and Egan TBP2 genes throught the *E. coli* lpp leader

Nde I

TATGAAAGCTACTAAACTGGTTCGGGTGCTGTTTATCCTGGGTCCACTCG...
ACTTTTCGATGATTTGACCAAGACCCACGACAATAGGACCCCAAGGTGAGAC...

Ear I

...CTGGCTGGTTGTAGCGGAGGTGGTGTGTTTTTGATGTAGATAACGTCTCTAATACCCCTCTTCT
...GACCCACCAACATCGCTCCACCAACAAACTACATCTATTCAGAGATTATGGGGGAGAAGATT

FIG.20B.

Oligonucleotide pair C (Seq. ID 90 and 91) to join the T7 promoter and Egan TBP2 genes through the *E. coli* rib B leader

Nde I

TATGCCATATCTGCCAACATGTGTTATCTCTGGCGGTGTTAATCACCGCTG...
ACGCTATAGACCGTTGTAAACAATAGAGACCGCCACAATTAGTGGCGAC...

Ear I

...CTTGTAGCGGAGGTGTTCTTTTGTATGATAGATAACGTCTCTAATACCCCTCTTCT
...CAACATCGCTCCACCAAGAAACTACATCTATTGCAGAGATTATGGGGGAGAAGATTT

Oligonucleotide pair D (Seq. ID 92 and 93) to join the T7 promoter and Egan TBP2 genes through the *E. coli* pal leader

Nde I

TATGCAACTGAACAAAGTGTGAAGGCTGATGTTGCTCTGCCGTGTTATGGCAA...
ACGTTGACTTGTTTCACGACTTTCGCCACTACTAAGGAGACGGACAATACCGTT...

Ear I

...TTGCTGTTTGTAGCGGAGGTGTTCTTTTGTATGATAGATAACGTCTCTAATACCCCTCTTCT
... AACGACCAACATCGCTCTCCACCAAGAAACTACATCTATTGCAGAGATTATGGGGGAGAAGATTT

ATG start codons are underlined

TGT coding for Cys of lipoproteins are double underlined

TGT may be replaced by TCC coding for Ser to secrete non-lipoprotein

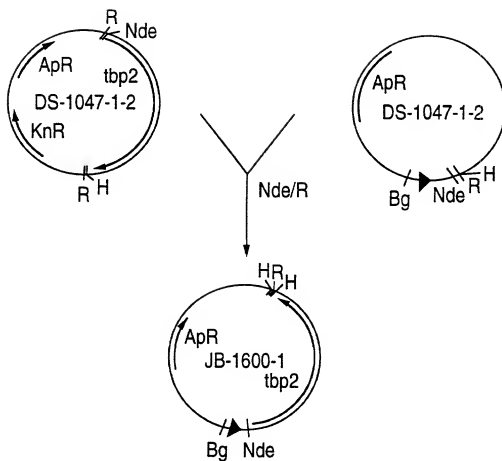


FIG.21.

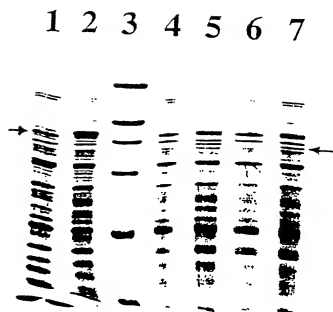


FIG.22.

PURIFICATION OF rTBP1/ rTBP2 FROM *E. COLI*

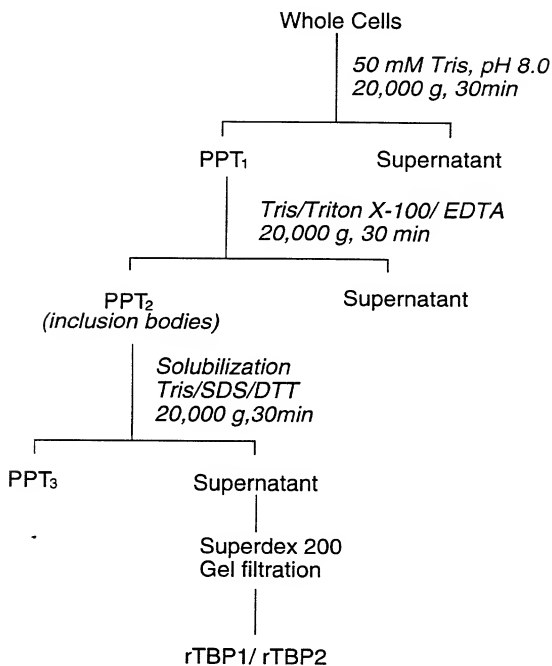
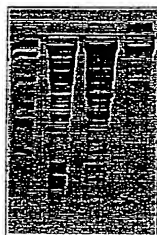


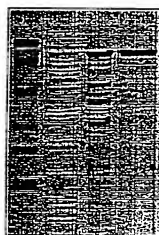
FIG.23.

rTBP1



1 2 3 4

rTBP2



1 2 3 4

FIG 24

Kinetics of Antibody Response to TBP1/TBP2 in Mice

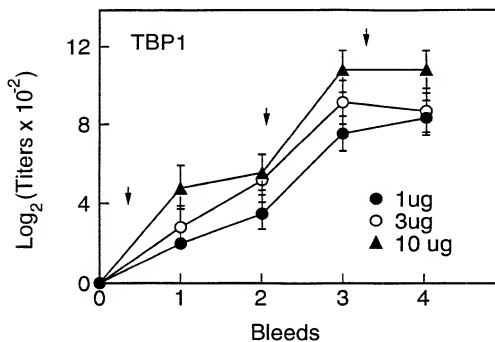


FIG.25 A.

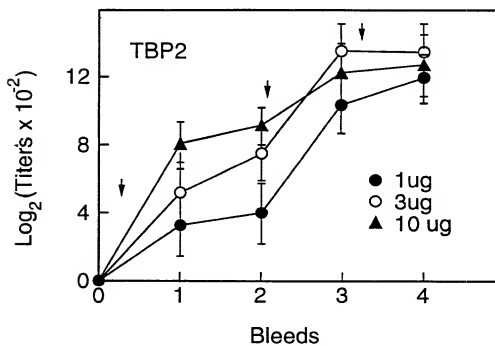


FIG.25 B.

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15

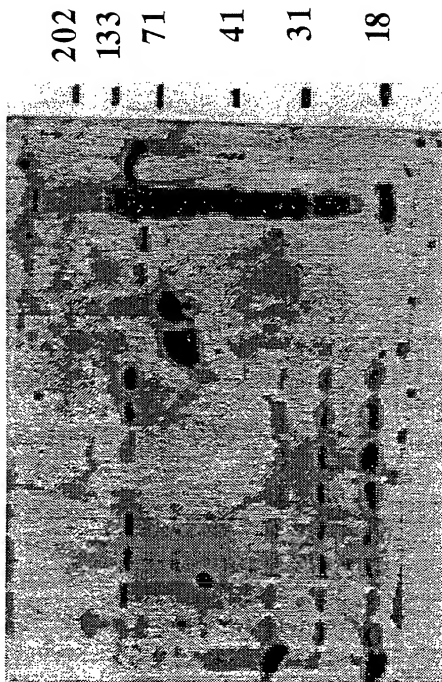


FIG.26.

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15

202

133

71

42

30

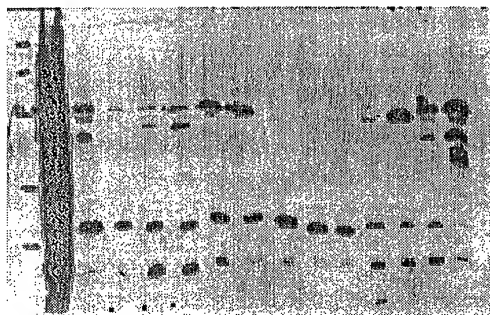
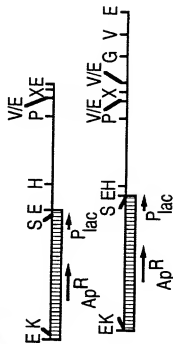
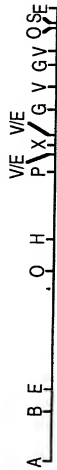


FIG. 27.

Construction of plasmids pUHIT1KFH and pUHIT1KFP

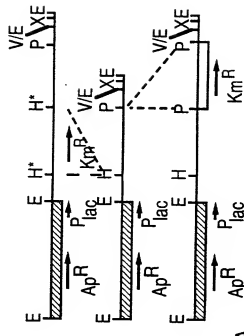
DL63 Wild Type
Chromosomal Map



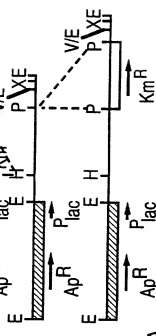
pBHIT1



pBHIT2



pBHIT1KFH



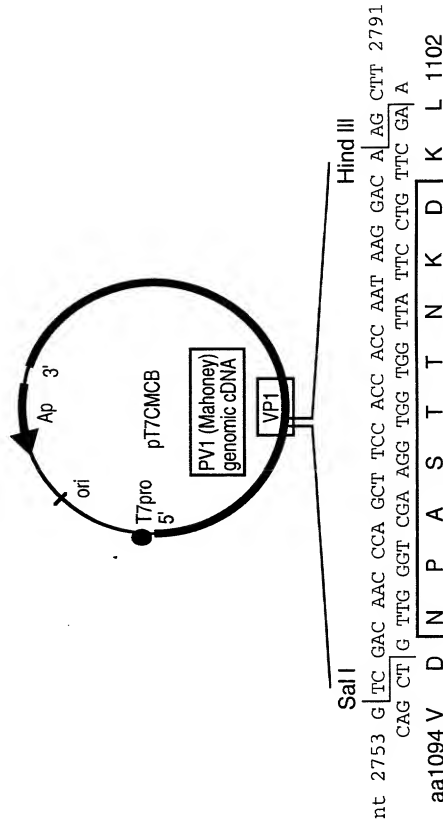
pBHIT1

pBHIT1KFP

- chromosomal DNA
- pBluescript SK+
- pUC4K
- pUC4K Km^R cassette

1kb

FIG.28.



Clone	Sequence encoded	SEQ.	Viability virus
pT7XLD	NPASTTNKD	132	Yes/PV1-XLD
pT7TBP2A	NPASTTSLEGGFYGPKD	133	Yes/PV1TBP2A
pT7TBP2B	NPASTTSLEGGFYGKD	134	Yes/PV1TBP2B
pT7TBP2C	NPASTTLEGGFYGPKD	135	Yes/PV1TBP2C
pT7TBP2D	NPASTTLEGGFYGKD	136	Yes/PV1TBP2B

FIG.29.

FIG.30.

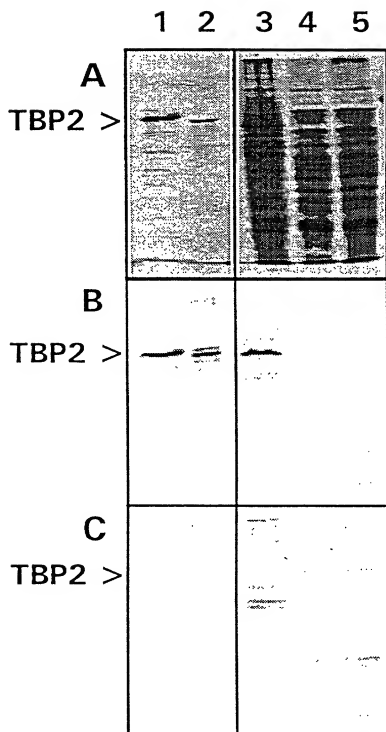


FIG.31A

Eagan Tbp2

MKSVPLISGGLSFLLSACS[↓]GGGFVDVNSNTPSSKPRYQDDTSNQRKKS

Signal Sequence

DS-1466-1-18



NLKKLFIPSLGGMKLVAQNLRGNKEPSFLNEDDYISYFSSLSTIEKDVK

DS-1466-4-3



DNKNKGADLIGSIDEPTTNPPEKHHGQKYVYSGLYYTPSWSLNDSKNKF

YLGYYGYAFYYGNKTATNLPVNGVAKYKGTWDFITATKNGKRYPLL[↓]SNGS

HAYYRRSAIPEDIDLENSKNGDIGLISEFSADFGTKKLTGQLSYTKRKT

DS-1466-5-1



NNQPYEKKKLYDIDADIYSNRFRGTVPKTEKDSEHPFTSEGTLEGGFYG

DS-1466-4-1



PNAEELGGKFLATDNRVFGVFSAKETEETKKEALSKETLIDGKLITFSTK

FIG. 31B

FIG.31B DS-1457-3-1
↓
KTDAKTNATSTAANTTTDTTANTTTDEKNFKTEDISSFGEADYLLIDKY
DS-1466-1-4 DS-1466-7-9 DS-1466-3-1 DS-1466-3-4
↓ ↓ ↓ ↓ ↓
PIPLLDPKNTNDFISSKHHITVGNKRYKVEACCSNLSYVKFGMYEDPLKE
DS-1466-2-6
↓
KETETETETEKDEKEKEKDDKEKQATAATTNTYYQFLLGHRTPKDDIPK
DS-1461-1-1 DS-1466-1-14 DS-1466-1-1
↓ ↓ ↓
TGSAKYHGSWFGYITDGKTSYSPSGDKKRDKNVAEFNVDFAEKKLTGEL
↓
KRHDTGNPVSIEANFNSSNAFTGTATATNFVIDGKNSQNKNTPINITTT
DS-1461-8-1
↓
KVNGA FYGPKASELGGYFTYNGNSTATNSESSSTVSSSSNSKNARAAVVF
↓
GAROOVETTK *

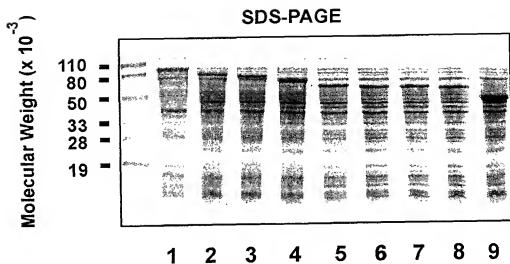


FIG 32 A.

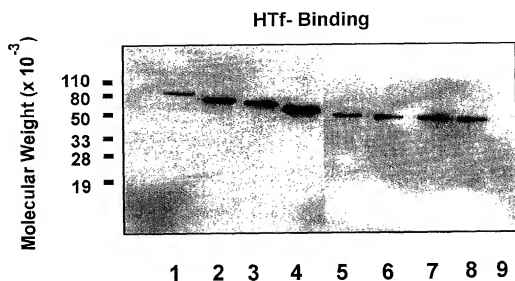


FIG 32 B.